



# wwPDB EM Validation Summary Report ⓘ

Jan 24, 2023 – 08:08 PM EST

PDB ID : 4V7E  
EMDB ID : EMD-1780  
Title : Model of the small subunit RNA based on a 5.5 Å cryo-EM map of *Triticum aestivum* translating 80S ribosome  
Authors : Barrio-Garcia, C.; Armache, J.-P.; Jarasch, A.; Anger, A.M.; Villa, E.; Becker, T.; Bhushan, S.; Jossinet, F.; Habeck, M.; Dindar, G.; Franckenberg, S.; Marquez, V.; Mielke, T.; Thomm, M.; Berninghausen, O.; Beatrix, B.; Soeding, J.; Westhof, E.; Wilson, D.N.; Beckmann, R.  
Deposited on : 2013-11-22  
Resolution : 5.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

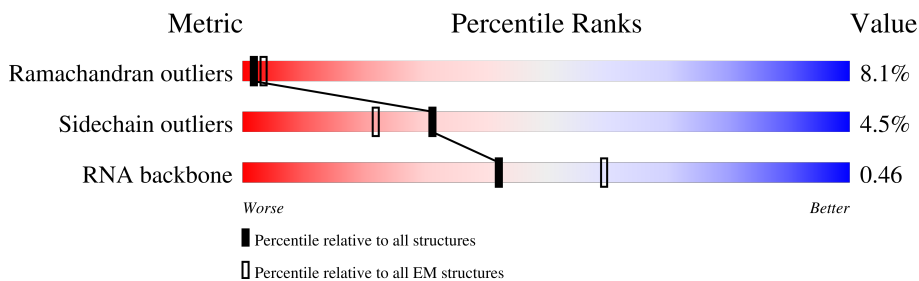
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	Ad	1810	<div style="display: flex; justify-content: space-between;"> <div style="text-align: right;">9%</div> <div style="text-align: left;">69%</div> <div style="text-align: right;">24%</div> </div>
2	Ae	75	<div style="display: flex; justify-content: space-between;"> <div style="text-align: right;">29%</div> <div style="text-align: left;">71%</div> <div style="text-align: right;">25%</div> </div>
3	Af	11	<div style="display: flex; justify-content: space-between;"> <div style="text-align: right;">9%</div> <div style="text-align: left;">82%</div> <div style="text-align: right;">73%</div> </div>
4	BY	138	<div style="display: flex; justify-content: space-between;"> <div style="text-align: right;">51%</div> <div style="text-align: left;">88%</div> <div style="text-align: right;">10%</div> </div>
5	BI	220	<div style="display: flex; justify-content: space-between;"> <div style="text-align: right;">14%</div> <div style="text-align: left;">28%</div> <div style="text-align: right;">70%</div> </div>
6	BK	183	<div style="display: flex; justify-content: space-between;"> <div style="text-align: right;">26%</div> <div style="text-align: left;">44%</div> <div style="text-align: right;">5%</div> </div>
7	BM	171	<div style="display: flex; justify-content: space-between;"> <div style="text-align: right;">47%</div> <div style="text-align: left;">61%</div> <div style="text-align: right;">9%</div> </div>
8	Bf	155	<div style="display: flex; justify-content: space-between;"> <div style="text-align: right;">25%</div> <div style="text-align: left;">35%</div> <div style="text-align: right;">11%</div> </div>

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Mol	Chain	Length	Quality of chain
9	BX	142	48% 95% ..
10	Bg	380	77% 92% 7% .
11	BD	208	58% 75% 23% .
12	BE	265	32% 70% 5% 25%
13	BF	191	38% 92% 7% .
14	BQ	149	40% 68% 14% 15%
15	BU	128	59% 87% 10% .
16	BO	151	41% 67% 11% 21%
17	BS	152	48% 78% 20% .
18	BN	151	45% 66% 13% 20%
19	BL	160	31% 46% 7% 47%
20	BT	146	44% 89% 8% .
21	BP	154	29% 51% 5% 41%
22	BZ	108	49% 77% 11% 5% 7%
23	Bc	65	60% 66% 18% 5% 11%
24	BW	130	56% 86% 12% .
25	Bd	56	50% 62% 16% 7% 14%
26	Bb	86	49% 94% 6%
27	Be	62	58% 89% 8% .
28	BA	260	42% 69% 7% 24%
29	BR	141	50% 73% 9% 18%
30	BB	262	38% 69% 11% 19%
31	BV	82	57% 84% 9% 7%
32	Ba	133	26% 59% 11% 30%
33	BJ	195	31% 90% 6% . .

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Mol	Chain	Length	Quality of chain
34	BC	263	44% 77% 19%
35	BG	245	43% 88% 5% • 6%
36	BH	189	52% 83% 12% • • •
37	CG	257	38% 84% 8% 8%
38	CT	164	47% 85% 12% •
39	CZ	136	33% 96% •
40	Cz	216	98% 92% 8%
41	CA	261	54% 86% 10% • •
42	CJ	180	34% 78% 12% • • 6%
43	CH	190	41% 93% 6% •
44	CV	140	74% 93% 7%
45	CN	200	35% 89% 8% •
46	Ca	144	50% 77% 22% • •
47	CQ	188	39% 73% 12% • • 13%
48	CD	304	37% 75% 18% 6% •
49	CR	209	44% 80% 8% • 10%
50	CP	171	42% 86% 12% •
51	CX	152	40% 73% 6% • 20%
52	CW	162	31% 43% • • 54%
53	CY	150	21% 79% 6% • 13%
54	Cr	147	18% 42% 6% • 50%
55	Cc	112	45% 92% 7% •
56	Cd	123	46% 84% 12% • • •
57	Ce	133	58% 89% 8% •
58	Cj	94	39% 80% 19% •

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Mol	Chain	Length	Quality of chain
59	Cl	51	47% 86% 12%
60	Co	105	48% 79% 18%
61	CM	134	35% 83% 14%
62	CS	178	37% 76% 14% 6%
63	CU	130	53% 62% 15% 5% 17%
64	Ci	112	31% 55% 11% 31%
65	CK	166	73% 65% 10% 23%
66	Cu	110	53% 51% 47%
66	Cv	110	53% 52% 47%
67	Cs	113	52% 51% 48%
67	Ct	113	52% 50% 48%
68	Ch	124	40% 89% 10%
69	CF	244	41% 92% 7%
70	Cq	319	76% 76% 5% 18%
71	CB	389	44% 83% 14%
72	CC	405	45% 81% 8% 8%
73	CO	206	42% 88% 8%
74	Cp	92	50% 95% 5%
75	CI	224	36% 74% 8% 18%
76	Cn	25	72% 92% 8%
77	Cm	53	30% 94%
78	CL	208	40% 84% 12%
79	CE	219	53% 80% 15%
80	Cf	111	45% 94% 5%
81	Ck	69	45% 90% 10%

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Mol	Chain	Length	Quality of chain
82	Cb	60	57% 90% 10% 8%
83	Cg	119	41% 82% 10% 8%
84	Aa	3391	11% 71% 25%
85	Ac	160	5% 68% 28%
86	Ab	120	67% 32%

## 2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 212263 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	Ad	1762	37584	16788	6708	12327	1761	0	0

- Molecule 2 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	Ae	75	1595	712	280	529	74	0	0

- Molecule 3 is a RNA chain called 5'-R(\*AP\*AP\*AP\*AP\*GP\*AP\*CP\*UP\*UP\*CP\*A)-3'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	Af	11	232	106	45	71	10	0	0

- Molecule 4 is a protein called 40S ribosomal protein S24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	BY	138	1108	703	212	189	4	0	0

- Molecule 5 is a protein called 40S ribosomal protein S8E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	BI	66	533	330	105	95	3	0	0

- Molecule 6 is a protein called 40S ribosomal protein S10E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	BK	96	818	535	137	143	3	0	0

- Molecule 7 is a protein called 40S ribosomal protein S12E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	BM	123	924	577	159	179	9	0	0

- Molecule 8 is a protein called 40S ribosomal protein S31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	Bf	71	577	367	107	98	5	0	0

- Molecule 9 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	BX	142	1103	698	214	187	4	0	0

- Molecule 10 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	Bg	380	2929	1813	530	567	19	0	0

- Molecule 11 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	BD	208	1629	1029	294	297	9	0	0

- Molecule 12 is a protein called 40S ribosomal protein S4E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	BE	200	1607	1030	290	283	4	0	0

- Molecule 13 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	BF	191	1489	928	281	273	7	0	0

- Molecule 14 is a protein called 40S ribosomal protein S9.



Mol	Chain	Residues	Atoms					AltConf	Trace
14	BQ	126	Total	C	N	O	S	0	0
			1017	648	195	170	4		

- Molecule 15 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BU	128	Total	C	N	O	S	0	0
			982	613	176	187	6		

- Molecule 16 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BO	119	Total	C	N	O	S	0	0
			899	550	178	167	4		

- Molecule 17 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BS	152	Total	C	N	O	S	0	0
			1240	772	248	213	7		

- Molecule 18 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BN	121	Total	C	N	O	S	0	0
			977	627	180	167	3		

- Molecule 19 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BL	85	Total	C	N	O	S	0	0
			688	435	134	115	4		

- Molecule 20 is a protein called 40S ribosomal protein S19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BT	146	Total	C	N	O	S	0	0
			1155	726	218	207	4		

- Molecule 21 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BP	91	Total	C	N	O	S	0	0
			711	457	130	120	4		

- Molecule 22 is a protein called 40S ribosomal protein S25E.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BZ	100	Total	C	N	O	S	0	0
			779	489	146	144			

- Molecule 23 is a protein called 40S ribosomal protein S28E.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Bc	58	Total	C	N	O	S	0	0
			454	281	86	84	3		

- Molecule 24 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BW	130	Total	C	N	O	S	0	0
			1042	667	189	181	5		

- Molecule 25 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Bd	48	Total	C	N	O	S	0	0
			379	233	77	63	6		

- Molecule 26 is a protein called 40S ribosomal protein S27E.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Bb	86	Total	C	N	O	S	0	0
			663	414	119	122	8		

- Molecule 27 is a protein called 40S ribosomal protein S30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Be	60	Total	C	N	O	S	0	0
			469	289	104	75	1		

- Molecule 28 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	BA	197	1537	969	280	278	10	0	0

- Molecule 29 is a protein called 40S ribosomal protein S17E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	BR	116	945	589	178	171	7	0	0

- Molecule 30 is a protein called 40S ribosomal protein S1E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	BB	211	1707	1089	308	302	8	0	0

- Molecule 31 is a protein called 40S ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	BV	76	601	371	112	115	3	0	0

- Molecule 32 is a protein called 40S ribosomal protein S26E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	Ba	93	753	461	163	122	7	0	0

- Molecule 33 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	BJ	187	1525	959	305	256	5	0	0

- Molecule 34 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	BC	214	1665	1074	297	287	7	0	0

- Molecule 35 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	BG	231	1867	1164	367	328	8	0	0

- Molecule 36 is a protein called 40S ribosomal protein S7E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	BH	184	1508	962	278	266	2	0	0

- Molecule 37 is a protein called 60S ribosomal protein L8E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	CG	237	1906	1226	351	322	7	0	0

- Molecule 38 is a protein called 60S ribosomal protein L21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	CT	160	1288	814	251	219	4	0	0

- Molecule 39 is a protein called 60S ribosomal protein L27E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	CZ	136	1090	704	205	176	5	0	0

- Molecule 40 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	Cz	216	1718	1092	309	304	13	0	0

- Molecule 41 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	CA	255	1946	1210	399	328	9	0	0

- Molecule 42 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	CJ	170	Total	C	N	O	S	0	0
			1380	869	256	246	9		

- Molecule 43 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CH	190	Total	C	N	O	S	0	0
			1500	947	270	277	6		

- Molecule 44 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CV	140	Total	C	N	O	S	0	0
			1048	658	199	181	10		

- Molecule 45 is a protein called 60S ribosomal protein L15E.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CN	194	Total	C	N	O	S	0	0
			1630	1027	342	257	4		

- Molecule 46 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ca	144	Total	C	N	O	S	0	0
			1114	710	223	175	6		

- Molecule 47 is a protein called 60S ribosomal protein L18E.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CQ	163	Total	C	N	O	S	0	0
			1284	810	248	219	7		

- Molecule 48 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CD	304	Total	C	N	O	S	0	0
			2444	1531	440	466	7		

- Molecule 49 is a protein called 60S ribosomal protein L19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	CR	189	1569	972	330	257	10	0	0

- Molecule 50 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	CP	171	1372	852	271	244	5	0	0

- Molecule 51 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	CX	122	987	634	178	173	2	0	0

- Molecule 52 is a protein called 60S ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	CW	75	635	408	126	97	4	0	0

- Molecule 53 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	CY	130	1048	647	220	178	3	0	0

- Molecule 54 is a protein called 60S ribosomal protein L28E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	Cr	73	576	364	107	103	2	0	0

- Molecule 55 is a protein called 60S ribosomal protein L30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	Cc	112	857	540	149	161	7	0	0

- Molecule 56 is a protein called 60S ribosomal protein L31E.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Cd	120	Total	C	N	O	S	0	0
			960	598	186	173	3		

- Molecule 57 is a protein called 60S ribosomal protein L32E.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ce	133	Total	C	N	O	S	0	0
			1103	696	216	185	6		

- Molecule 58 is a protein called 60S ribosomal protein L37E.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Cj	94	Total	C	N	O	S	0	0
			755	459	166	123	7		

- Molecule 59 is a protein called 60S ribosomal protein L39E.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Cl	51	Total	C	N	O	S	0	0
			460	291	100	67	2		

- Molecule 60 is a protein called 60S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Co	105	Total	C	N	O	S	0	0
			851	535	166	144	6		

- Molecule 61 is a protein called 60S ribosomal protein L14E.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	CM	134	Total	C	N	O	S	0	0
			1081	690	201	185	5		

- Molecule 62 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	CS	167	Total	C	N	O	S	0	0
			1419	916	263	233	7		

- Molecule 63 is a protein called 60S ribosomal protein L22E.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CU	108	Total	C	N	O	S	0	0
			864	551	155	156	2		

- Molecule 64 is a protein called 60S ribosomal protein L36E.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Ci	77	Total	C	N	O	S	0	0
			613	383	128	100	2		

- Molecule 65 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	CK	128	Total	C	N	O	S	0	0
			960	602	177	177	4		

- Molecule 66 is a protein called 60S ribosomal protein P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cu	58	Total	C	N	O	S	0	0
			432	283	69	79	1		
66	Cv	58	Total	C	N	O	S	0	0
			432	283	69	79	1		

- Molecule 67 is a protein called Acidic ribosomal protein P2.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Cs	59	Total	C	N	O	S	0	0
			441	278	69	90	4		
67	Ct	59	Total	C	N	O	S	0	0
			441	278	69	90	4		

- Molecule 68 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ch	124	Total	C	N	O	S	0	0
			1012	636	202	173	1		

- Molecule 69 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	CF	244	Total	C	N	O	S	0	0
			1984	1271	368	339	6		



- Molecule 70 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	Cq	262	1993	1278	330	377	8	0	0

- Molecule 71 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	CB	389	3139	1997	584	540	18	0	0

- Molecule 72 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	CC	372	2898	1823	556	510	9	0	0

- Molecule 73 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	CO	206	1650	1045	320	274	11	0	0

- Molecule 74 is a protein called 60S ribosomal protein L43E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	Cp	92	715	447	137	124	7	0	0

- Molecule 75 is a protein called 60S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	CI	184	1490	941	290	247	12	0	0

- Molecule 76 is a protein called 60S ribosomal protein L41E.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	Cn	25	238	145	62	28	3	0	0

- Molecule 77 is a protein called 60S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cm	52	Total	C	N	O	S	0	0
			428	267	90	66	5		

- Molecule 78 is a protein called 60S ribosomal protein L13E.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CL	208	Total	C	N	O	S	0	0
			1691	1061	338	286	6		

- Molecule 79 is a protein called 60S ribosomal protein L6E.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CE	219	Total	C	N	O	S	0	0
			1731	1106	314	307	4		

- Molecule 80 is a protein called 60S ribosomal protein L33E.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cf	111	Total	C	N	O	S	0	0
			891	561	170	156	4		

- Molecule 81 is a protein called 60S ribosomal protein L38E.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Ck	69	Total	C	N	O	S	0	0
			564	360	104	97	3		

- Molecule 82 is a protein called 60S ribosomal protein L29E.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Cb	58	Total	C	N	O	S	0	0
			477	288	103	85	1		

- Molecule 83 is a protein called 60S ribosomal protein L34E.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cg	110	Total	C	N	O	S	0	0
			897	567	182	146	2		

- Molecule 84 is a RNA chain called 60S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
84	Aa	3391	72601	32373	13241	23598	3389	0	0

- Molecule 85 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
85	Ac	160	3408	1522	614	1113	159	0	0

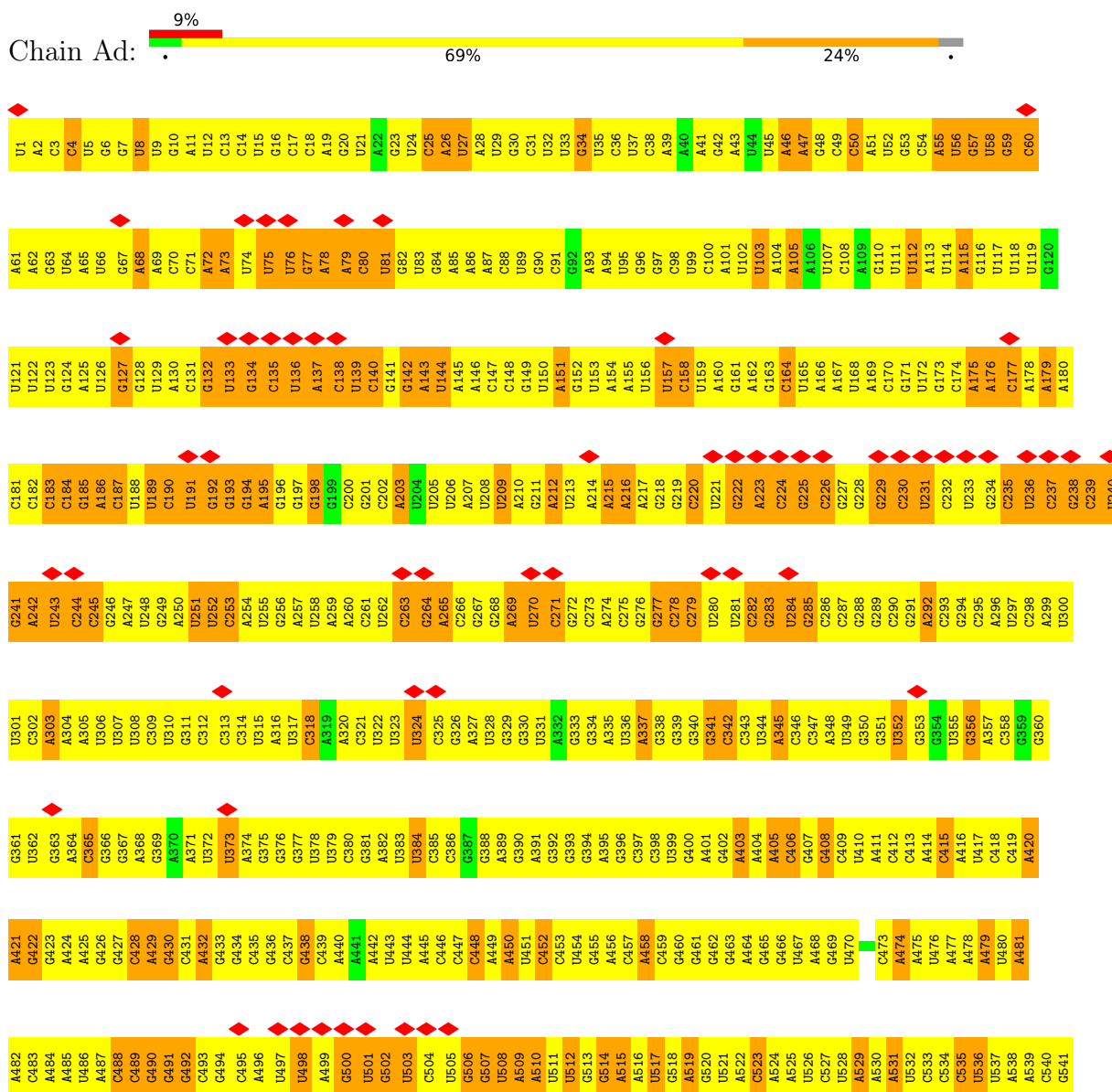
- Molecule 86 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
86	Ab	120	2561	1144	461	837	119	0	0

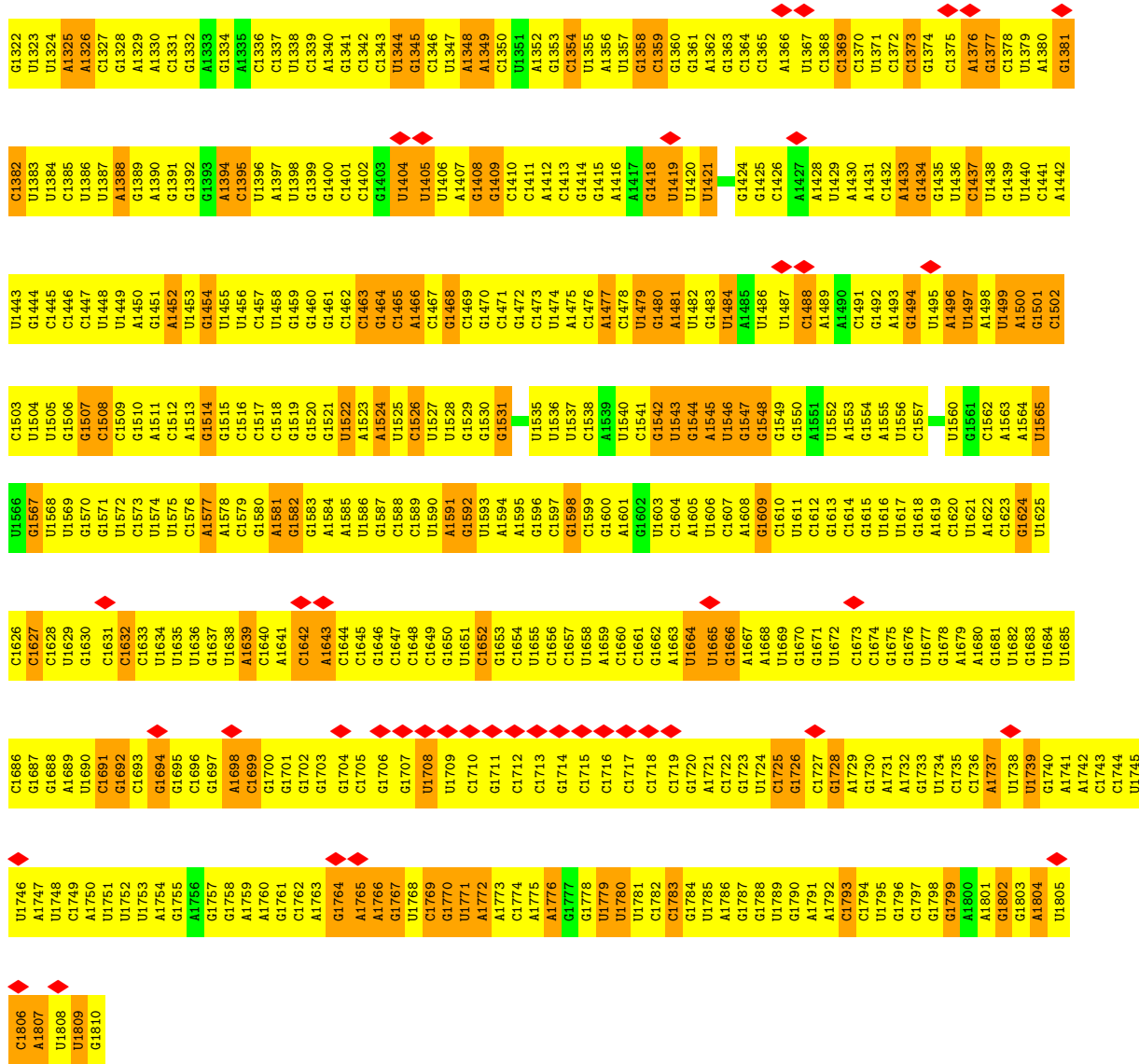
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

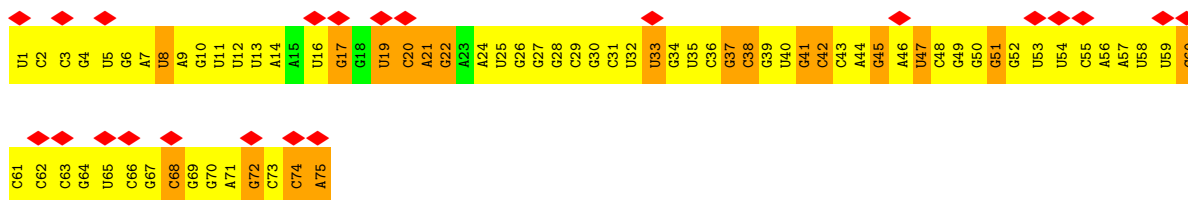
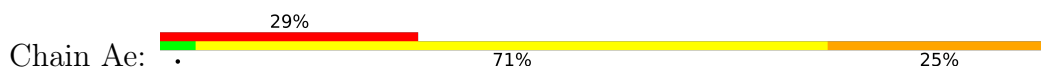
- Molecule 1: 18S ribosomal RNA



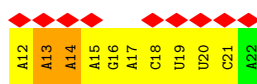
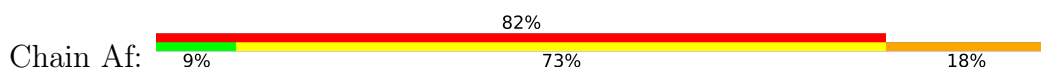
U1262	A1142	G1202	C1082	U1022	G962	C902	G842	A722	A642
C1263	A1143	G1203	C1083	C1023	U963	A903	C783	A723	G543
U1264	A1144	G1204	U1084	A1024	U964	G904	C784	U724	G544
A1265	G1145	U1205	U1085	A1025	U965	A905	A785	U725	A545
U1266	G1146	A1206	A1086	A1026	U966	G906	U786	G726	U646
G1267	A1147	A1207	U1087	C1027	C967	G907	C787	G727	C547
U1268	U1148	A1208	G1088	A1028	A968	U908	U788	A728	C548
G1269	U1149	C1209	A1089	U1029	C969	G909	G789	A729	A549
U1270	U1150	U1210	G1090	A1030	C949	A910	C789	C728	U550
G1271	A1151	A1211	A1091	A1031	A971	A911	U790	C729	G551
U1272	G1152	A1212	A1092	A1032	A972	A912	C791	G730	G552
C1273	C1153	C1213	A1093	U1033	U973	U913	U792	G731	G553
G1274	G1154	A1214	U1094	G1034	C974	U914	G793	A732	A554
U1275	G1155	A1215	C1095	A1035	A975	C915	G794	G733	G555
G1276	A1156	G1216	U1096	U1036	A976	U916	A795	U733	G556
U1277	A1157	G1217	A1097	G1037	G977	U917	U796	G734	G557
C1278	G1158	U1218	A1098	C1038	A978	G918	A797	A735	C558
U1279	G1159	C1219	U1099	C1039	A979	G919	C798	G735	A559
G1280	C1160	A1220	U1100	G1040	U979	G920	A799	U736	G560
U1281	G1161	A1221	C1101	A1041	U980	A920	U800	G737	G561
G1282	A1162	G1222	U1102	C1042	G981	U921	U801	A738	U562
C1283	C1163	A1223	U1103	C1043	A982	U922	A802	A739	C563
U1284	G1164	C1224	U1104	A1044	A983	U923	G803	A740	U564
G1285	A1165	A1225	U1105	G1045	A984	U924	C804	C741	G565
U1286	C1166	U1226	G1106	G1046	G985	U925	A805	C742	G566
U1287	C1167	A1227	U1107	G1047	U987	G926	U806	A743	G567
G1288	A1168	G1228	G1108	A1048	A988	A927	G807	G744	G568
U1289	G1169	C1229	U1109	U1049	G989	A928	G808	G745	C569
C1290	C1170	A1230	U1110	C1050	U990	A929	G809	G746	C570
U1291	G1171	G1231	C1111	G1051	G991	G930	A810	C747	A571
G1292	U1172	A1232	C1112	G1052	G992	C932	U811	U747	G572
U1293	G1173	C1233	G1113	C1053	U993	G933	A812	C748	C573
G1294	G1174	A1234	U1114	G1054	U994	A934	A813	A634	A574
U1295	A1175	U1235	G1115	G1055	C995	A935	C814	G635	G575
G1296	G1176	C1236	U1116	A1056	G996	C936	A815	U750	C576
U1297	G1177	G1237	G1117	U1057	A997	A937	U816	U751	C577
A1298	A1178	A1238	U1118	G1058	A998	A938	C817	A752	G578
C1299	C1179	C1239	G1119	U1059	G999	C939	A818	G639	C579
U1300	U1180	A1240	U1120	G1060	U1000	U940	A705	A640	G580
G1301	G1181	G1241	G1121	U1061	C1001	G941	U706	C641	A581
C1302	C1182	A1242	U1122	C1062	G1002	C942	U707	G642	U582
U1303	G1183	C1243	G1123	U1063	A1003	G943	G703	U643	A583
A1304	C1184	G1244	U1124	U1064	U1004	A944	C704	A644	A584
U1305	U1185	G1245	G1125	A1065	C1005	A945	A705	G645	U585
G1306	A1186	A1246	U1126	U1066	A1006	A946	U706	G646	U586
U1307	U1187	C1247	C1127	G1067	G1007	G947	A707	G647	C587
G1308	A1188	A1248	G1128	U1068	A1008	C948	G708	C648	C588
C1309	U1189	G1249	U1129	G1069	U1009	A949	C649	C649	A589
U1310	U1190	C1250	A1129	U1070	A1010	U950	C709	C650	G590
G1311	G1191	U1251	A1130	C1071	C1011	U951	G710	G651	C591
U1312	A1192	A1252	G1131	U1072	G1012	U952	C711	G	U
C1313	U1193	U1253	U1132	U1073	G1013	U953	U712	C	U
U1314	C1194	C1254	C1133	C1074	U1014	G954	A768	U	C
G1315	U1195	U1255	U1134	C1075	A955	C955	G769	C	G
U1316	C1196	C1256	G1135	G1076	U956	U956	U770	C	G
C1317	A1197	U1257	U1136	C1077	U1017	A957	G771	C	C
U1318	U1198	U1258	A1137	G1078	U1018	C958	A716	C	C
G1319	C1199	C1259	U1138	G1079	A1018	A959	G717	C	C
U1320	A1200	A1260	U1020	U1080	G1019	G959	C718	C	G
C1321	C1201	U1261	C1021	A1081	U1020	U960	A775	C	G
			U1141		C1021	G901	A776	U721	
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							C778		
							A780		
							A781		



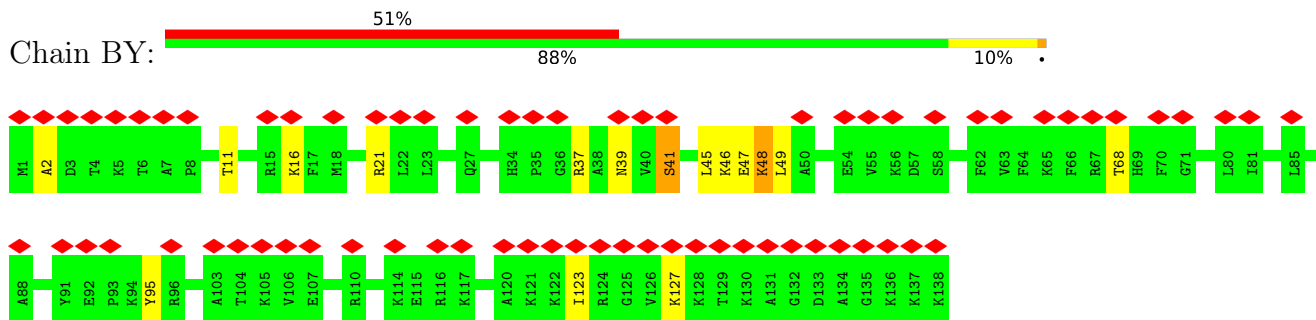
• Molecule 2: P-site tRNA



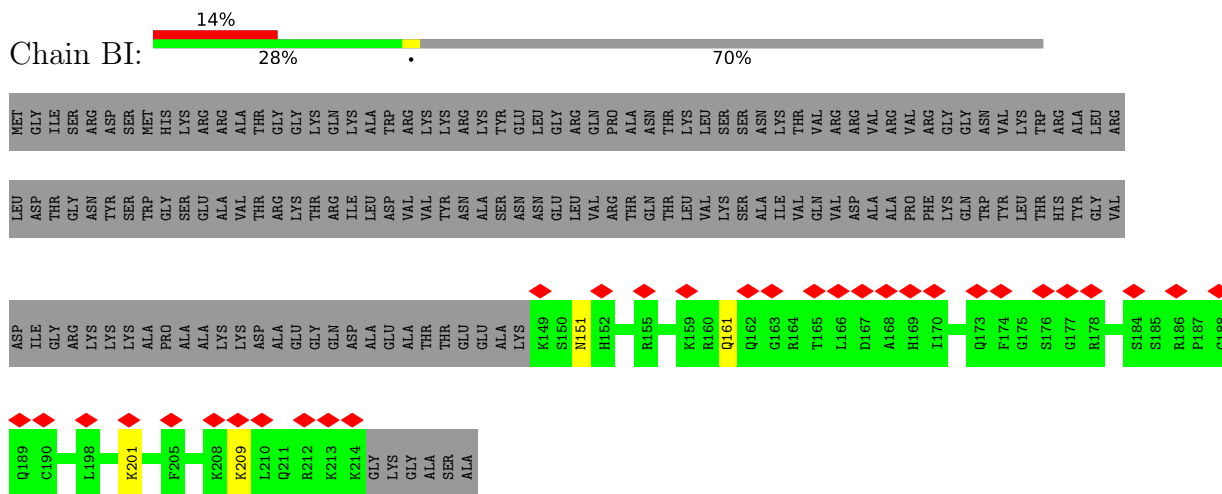
• Molecule 3: 5'-R(\*AP\*AP\*AP\*AP\*GP\*AP\*CP\*UP\*UP\*CP\*A)-3'



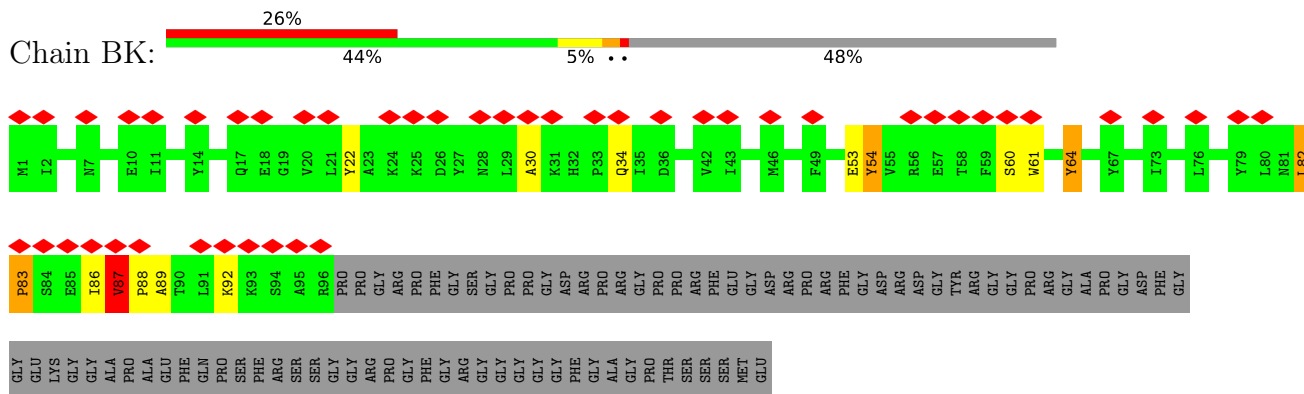
• Molecule 4: 40S ribosomal protein S24E



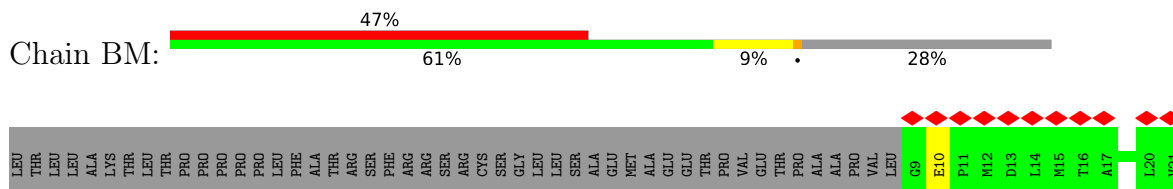
• Molecule 5: 40S ribosomal protein S8E

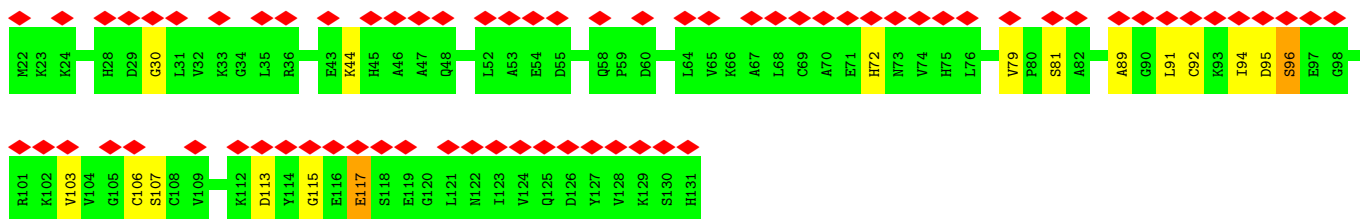


• Molecule 6: 40S ribosomal protein S10E

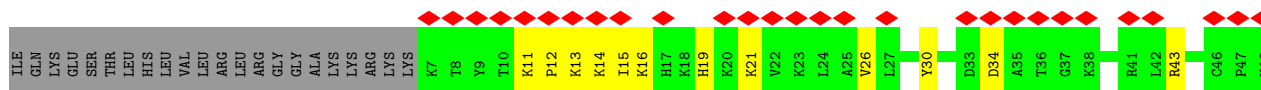
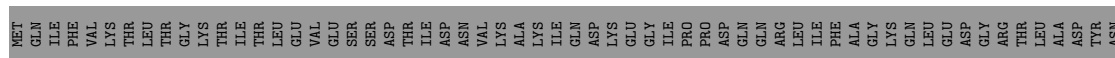
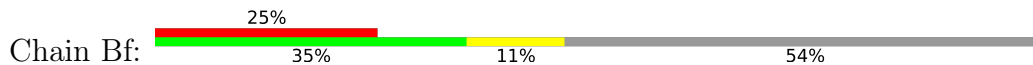


• Molecule 7: 40S ribosomal protein S12E

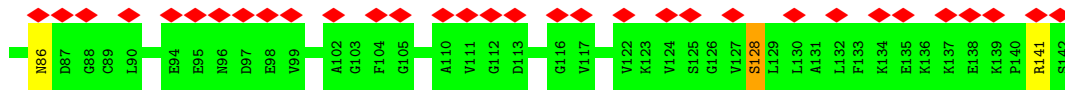
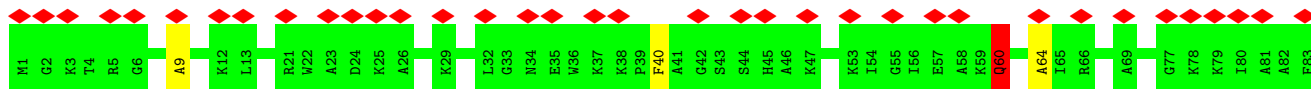




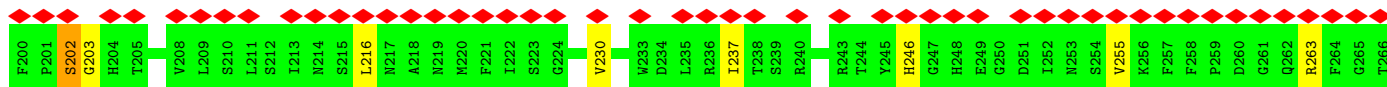
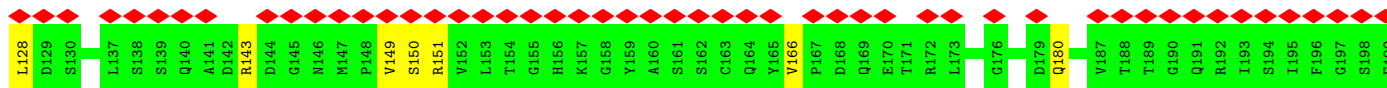
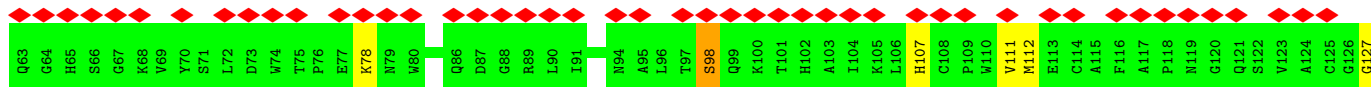
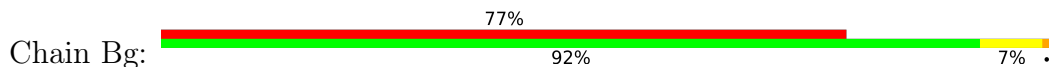
• Molecule 8: 40S ribosomal protein S31e



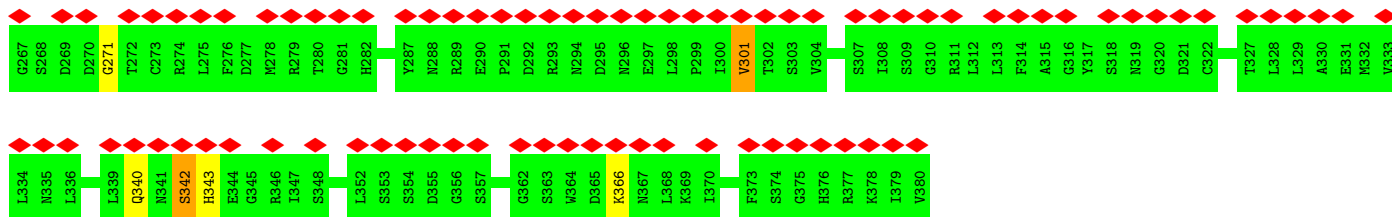
• Molecule 9: 40S ribosomal protein S12



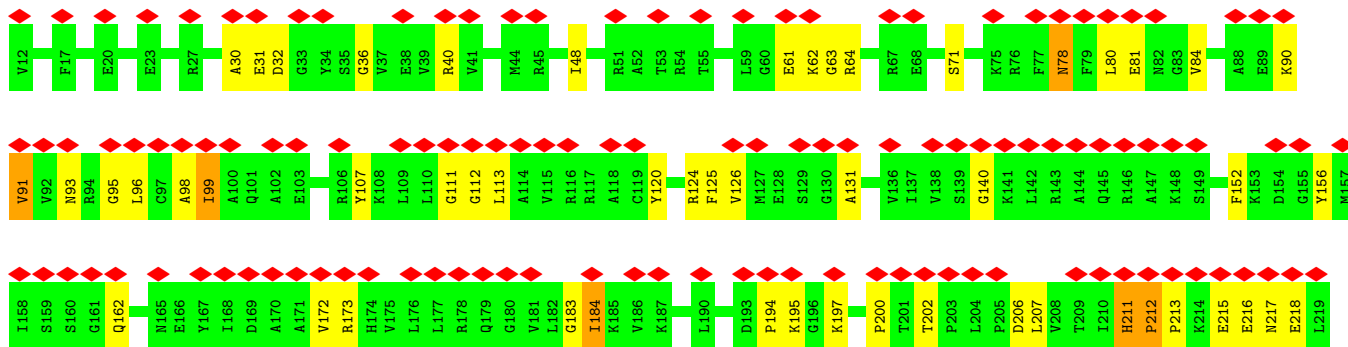
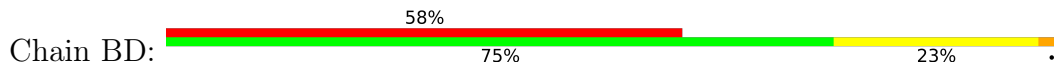
• Molecule 10: RACK1



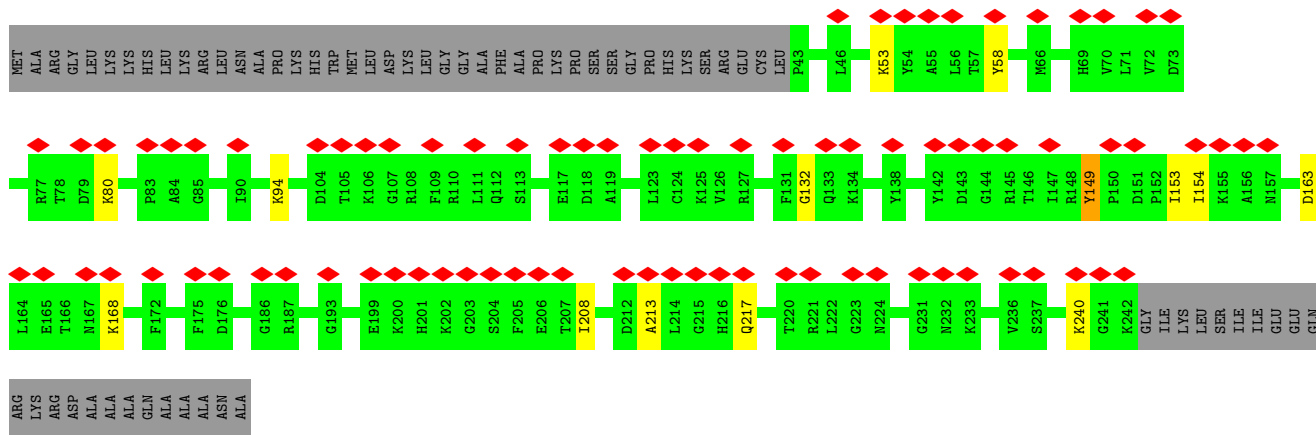




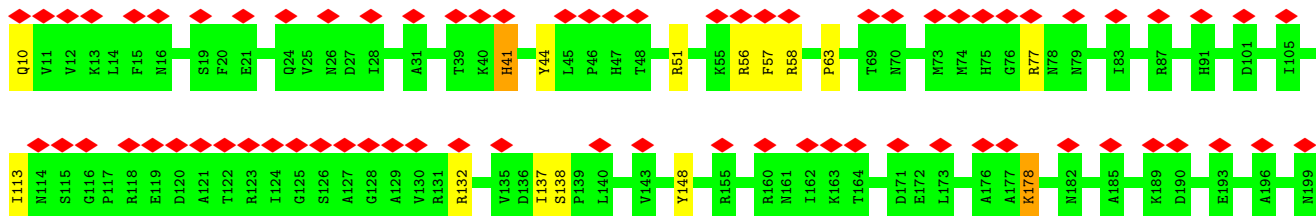
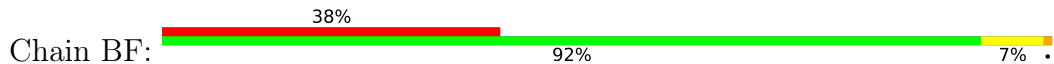
• Molecule 11: 40S ribosomal protein S3



• Molecule 12: 40S ribosomal protein S4E

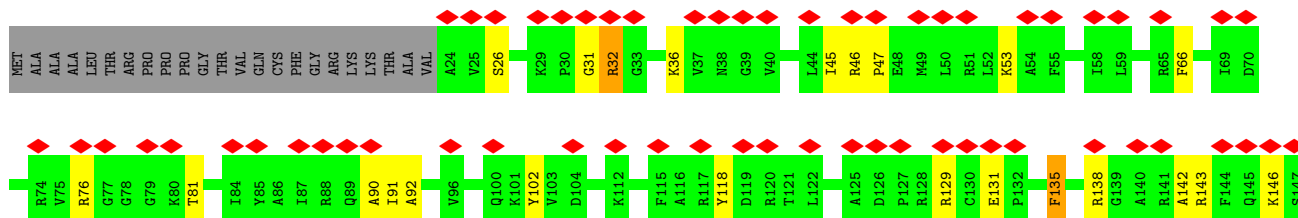
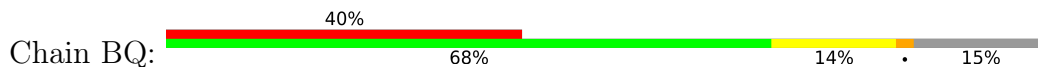


• Molecule 13: 40S ribosomal protein S7



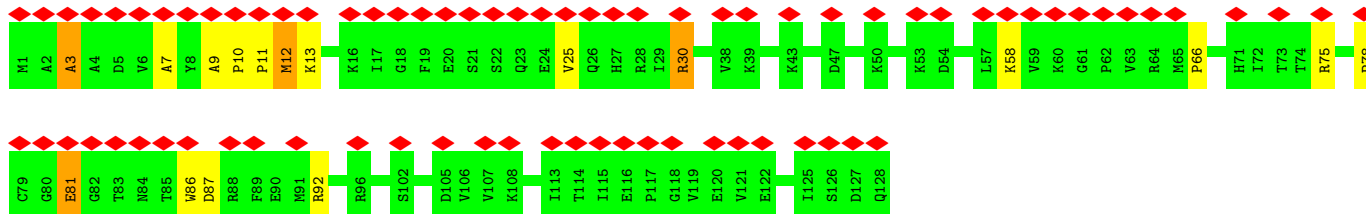
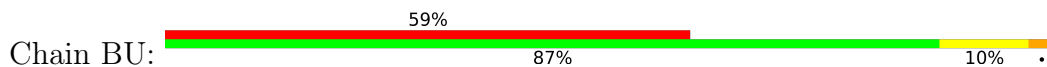
R200

- Molecule 14: 40S ribosomal protein S9

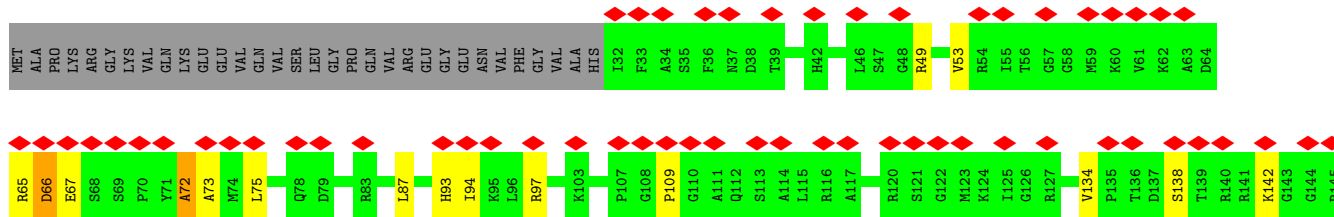
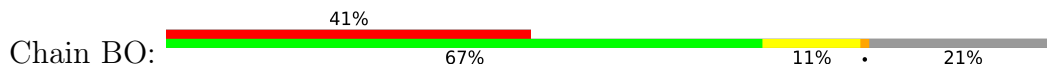


Y148 R149

- Molecule 15: 40S ribosomal protein S10

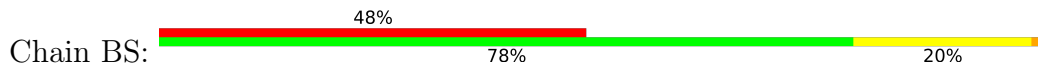


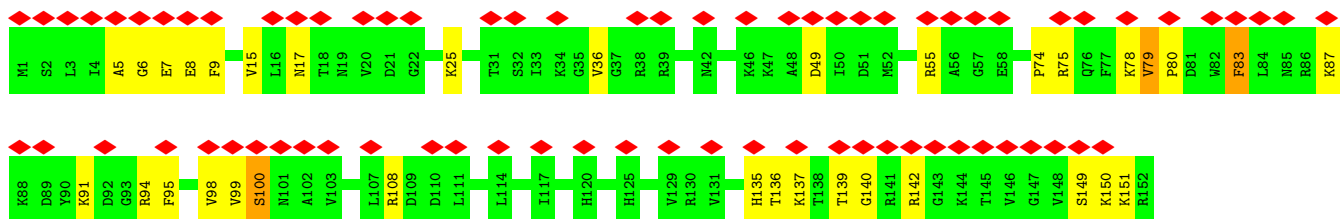
- Molecule 16: 40S ribosomal protein S11



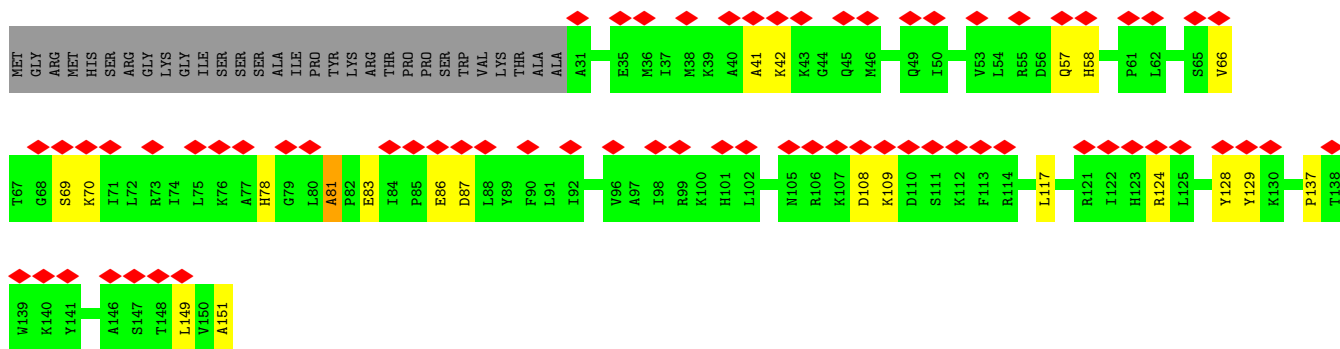
R146 G147 R148 R149 L150

- Molecule 17: 40S ribosomal protein S13

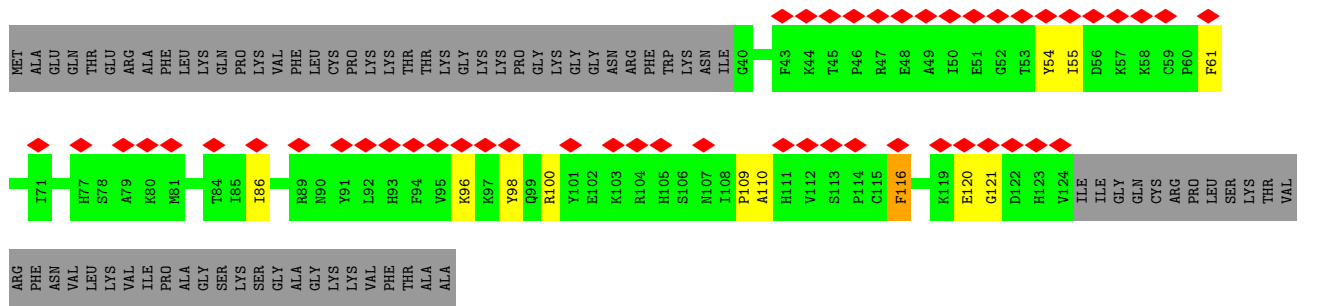




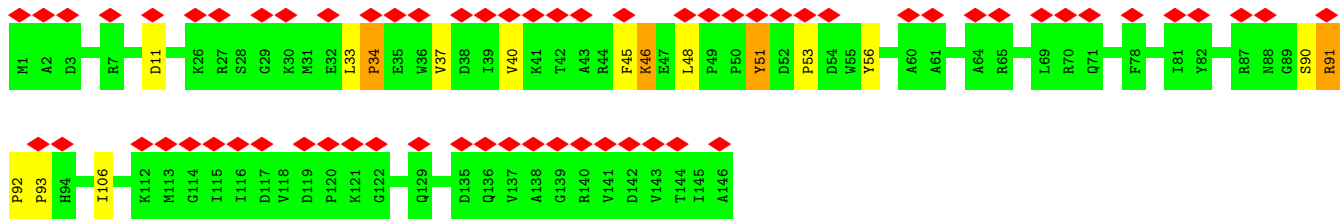
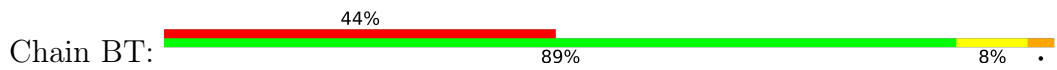
• Molecule 18: 40S ribosomal protein S15



• Molecule 19: 40S ribosomal protein S17



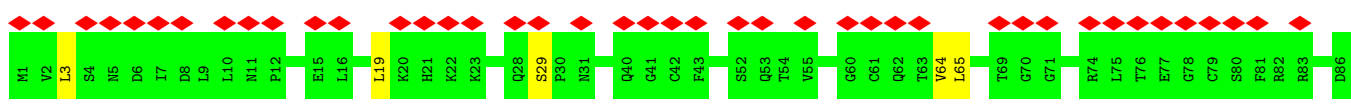
• Molecule 20: 40S ribosomal protein S19E



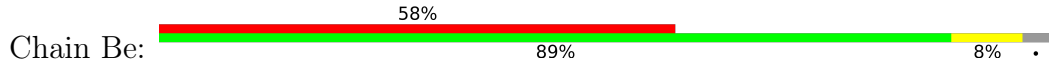
• Molecule 21: 40S ribosomal protein S19



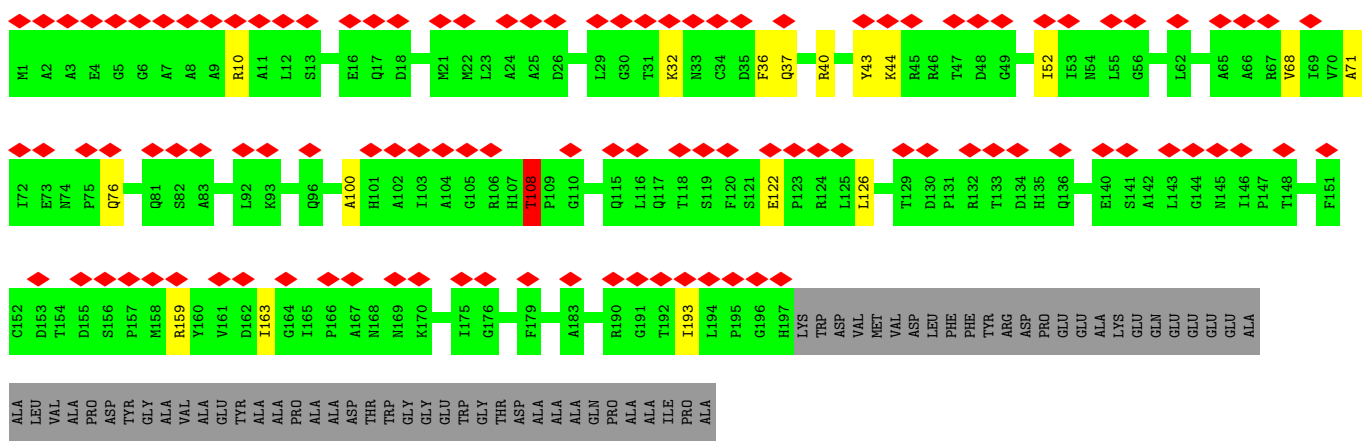
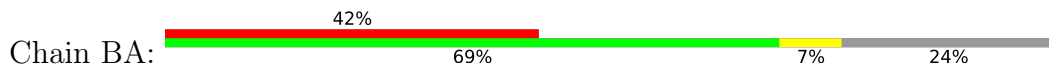




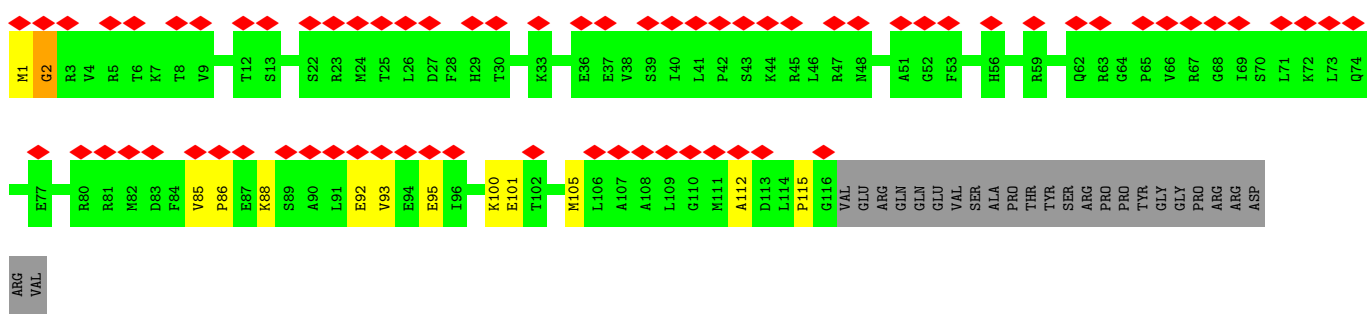
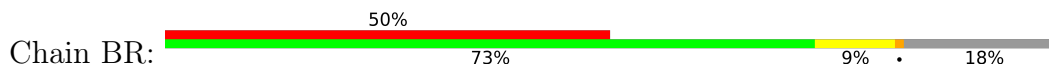
• Molecule 27: 40S ribosomal protein S30E



• Molecule 28: 40S ribosomal protein S2

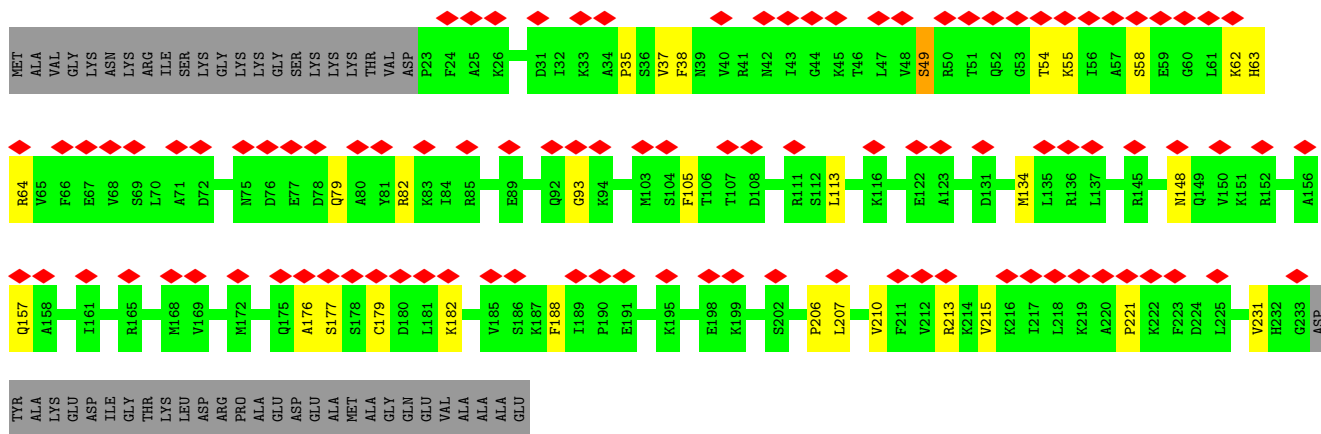


• Molecule 29: 40S ribosomal protein S17E

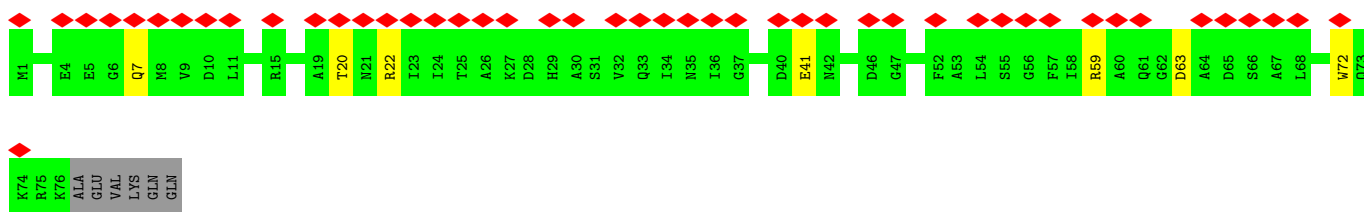
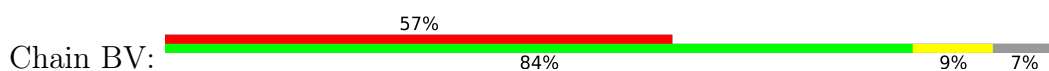


• Molecule 30: 40S ribosomal protein S1E

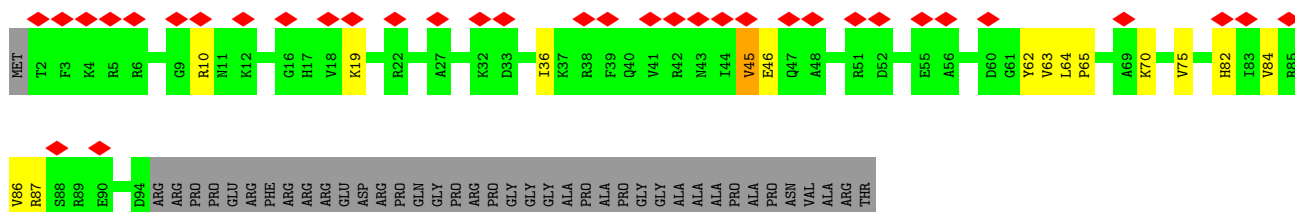




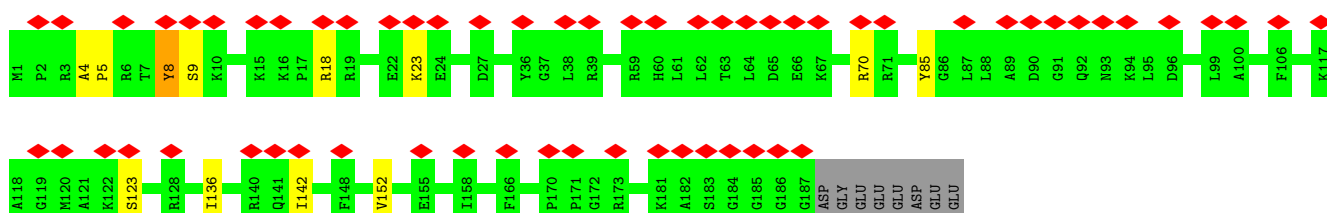
• Molecule 31: 40S ribosomal protein S21E



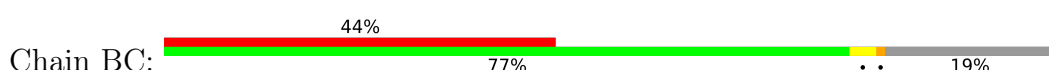
• Molecule 32: 40S ribosomal protein S26E



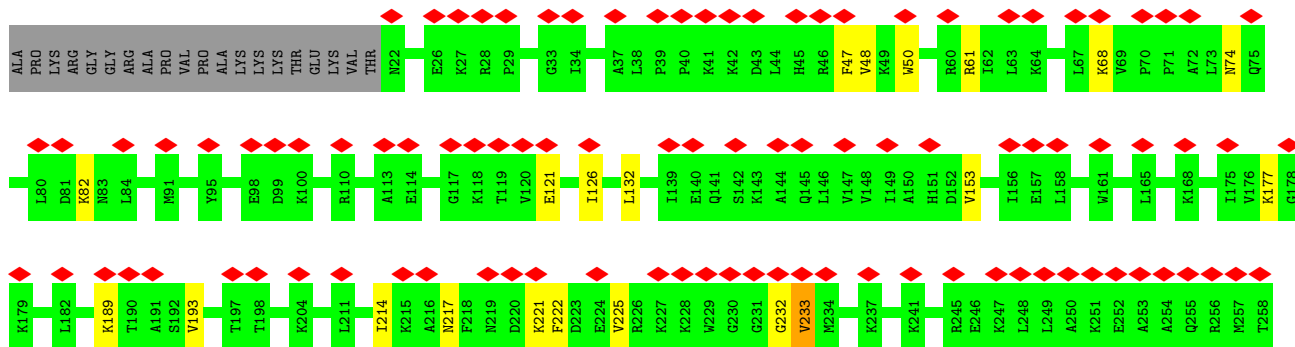
• Molecule 33: 40S ribosomal protein S4



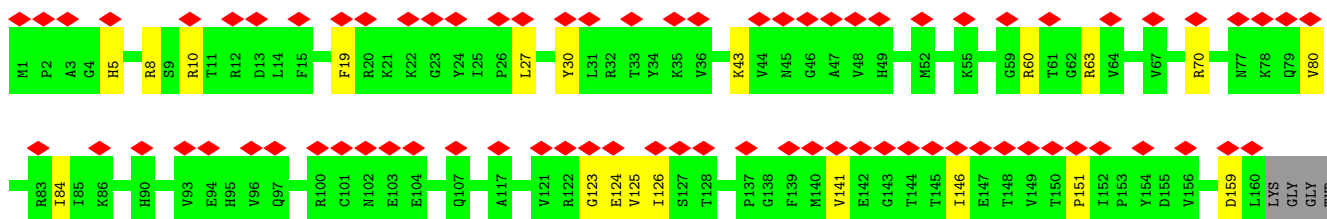
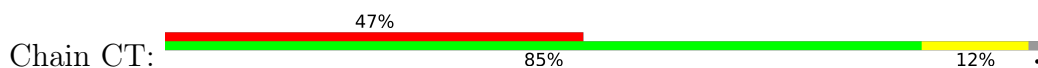
• Molecule 34: 40S ribosomal protein S5



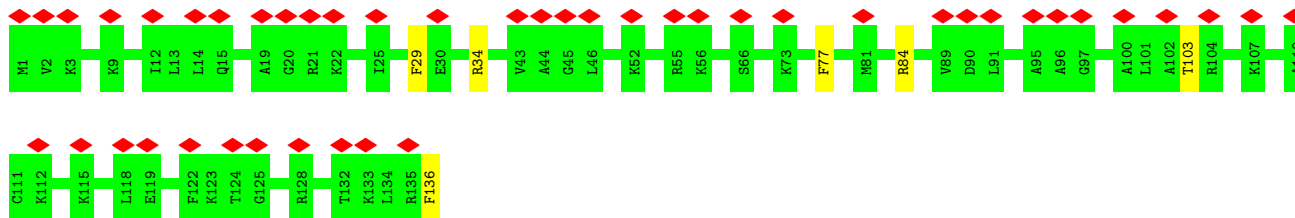




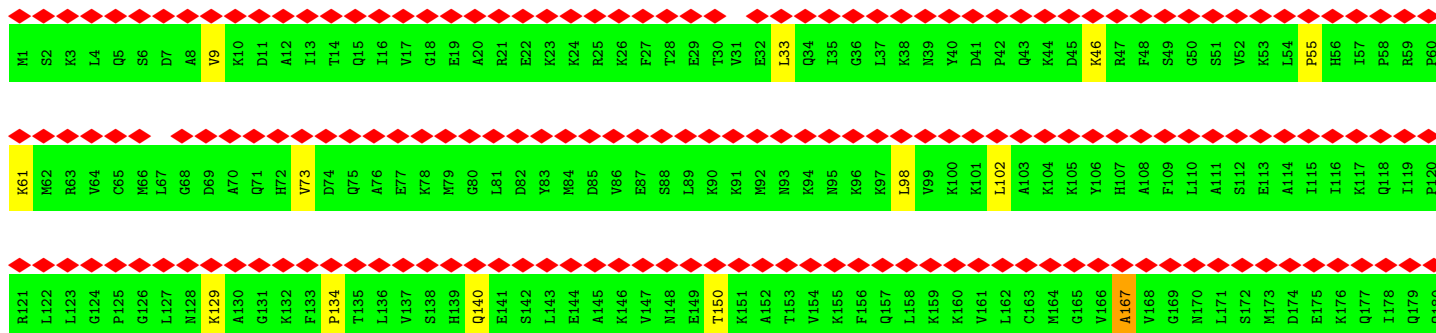
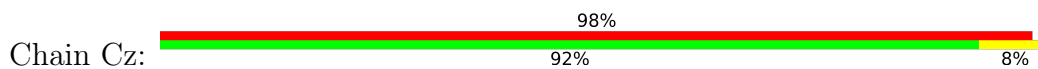
• Molecule 38: 60S ribosomal protein L21E



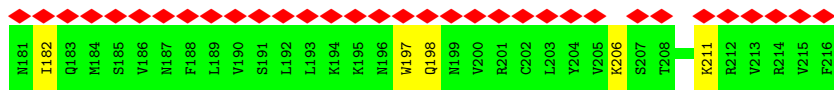
• Molecule 39: 60S ribosomal protein L27E



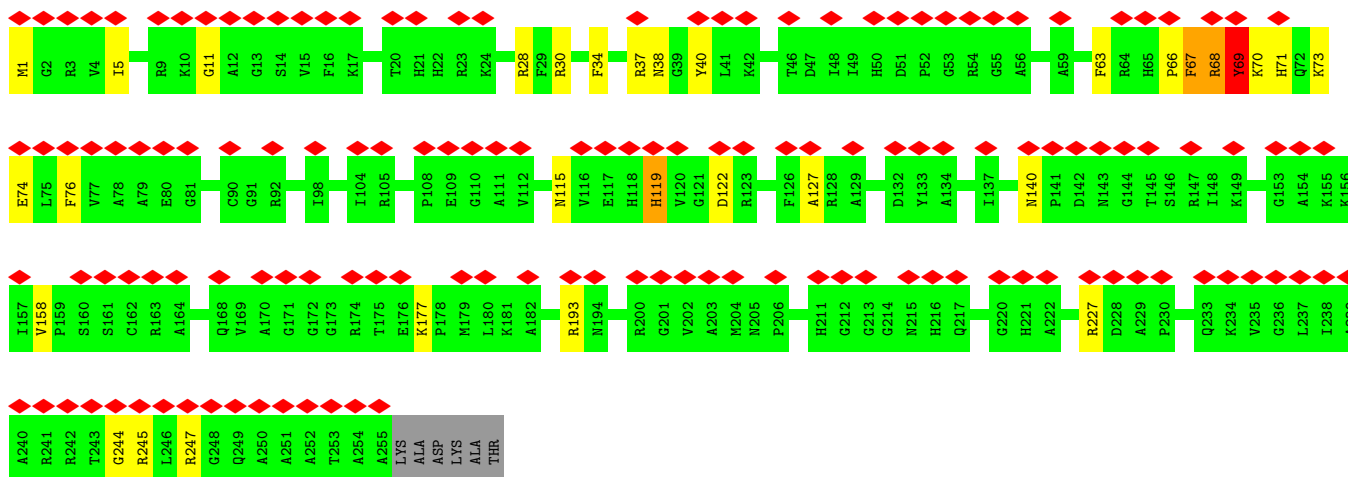
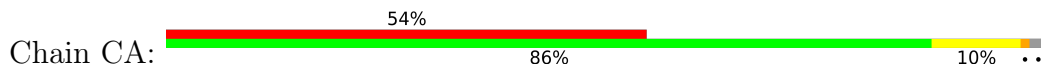
• Molecule 40: 60S ribosomal protein L1



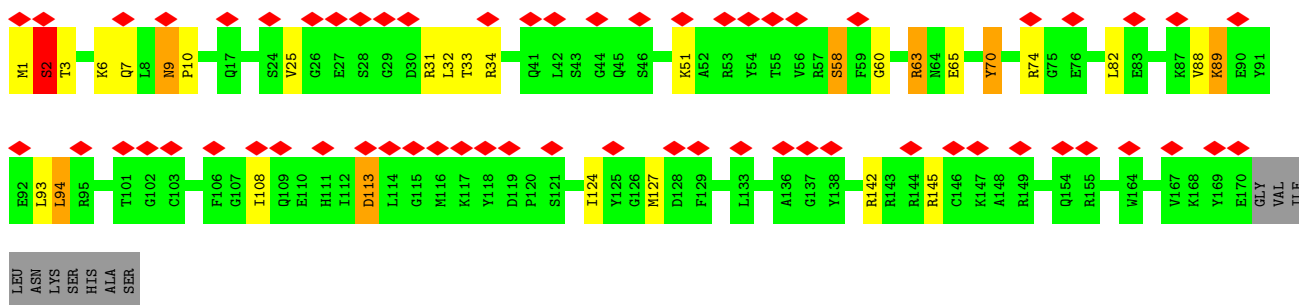
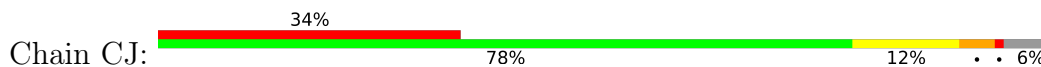




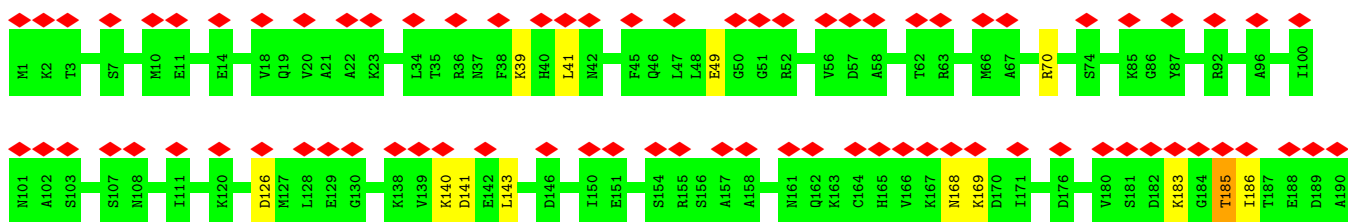
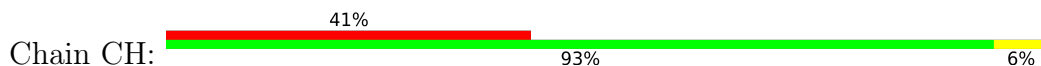
• Molecule 41: 60S ribosomal protein L2



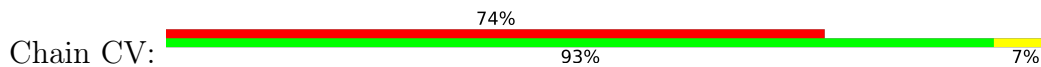
• Molecule 42: 60S ribosomal protein L5

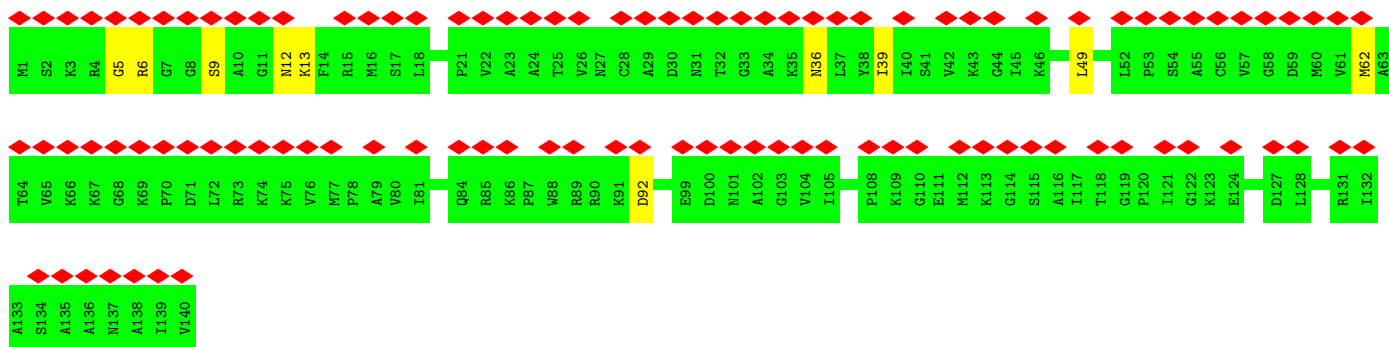


• Molecule 43: 60S ribosomal protein L6

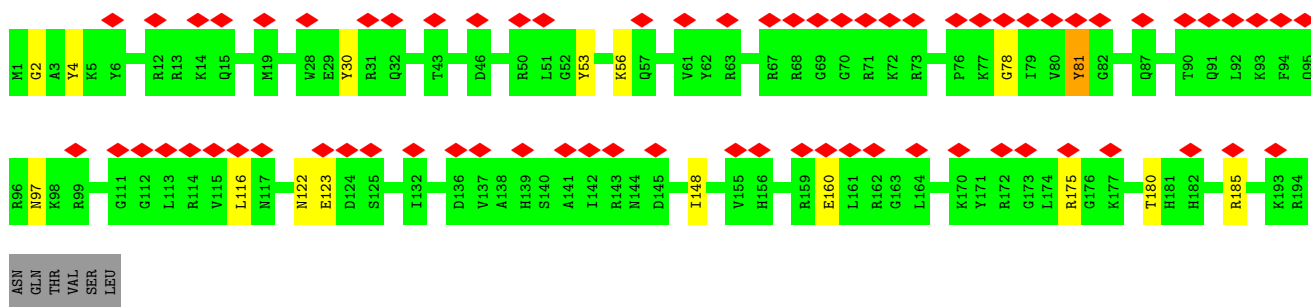
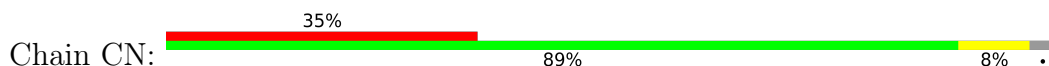


• Molecule 44: 60S ribosomal protein L14

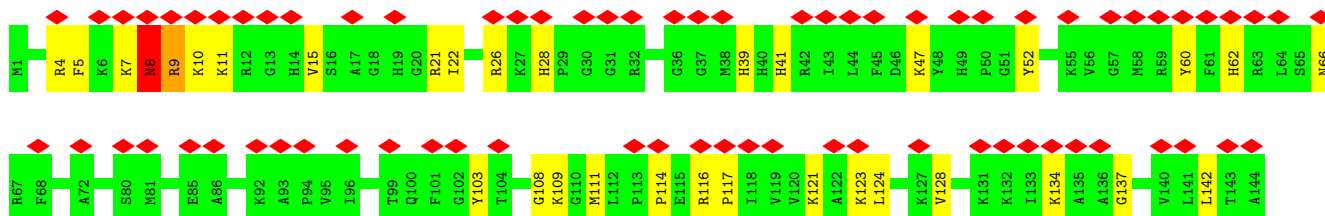
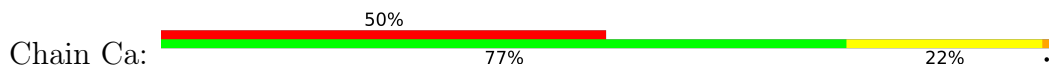




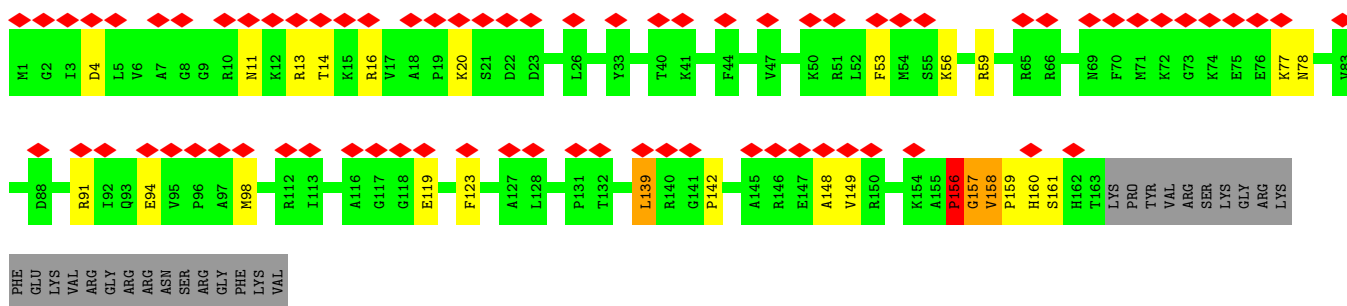
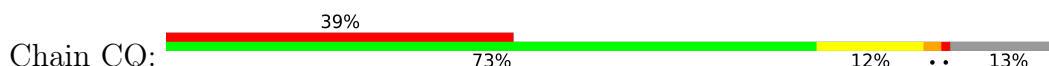
• Molecule 45: 60S ribosomal protein L15E



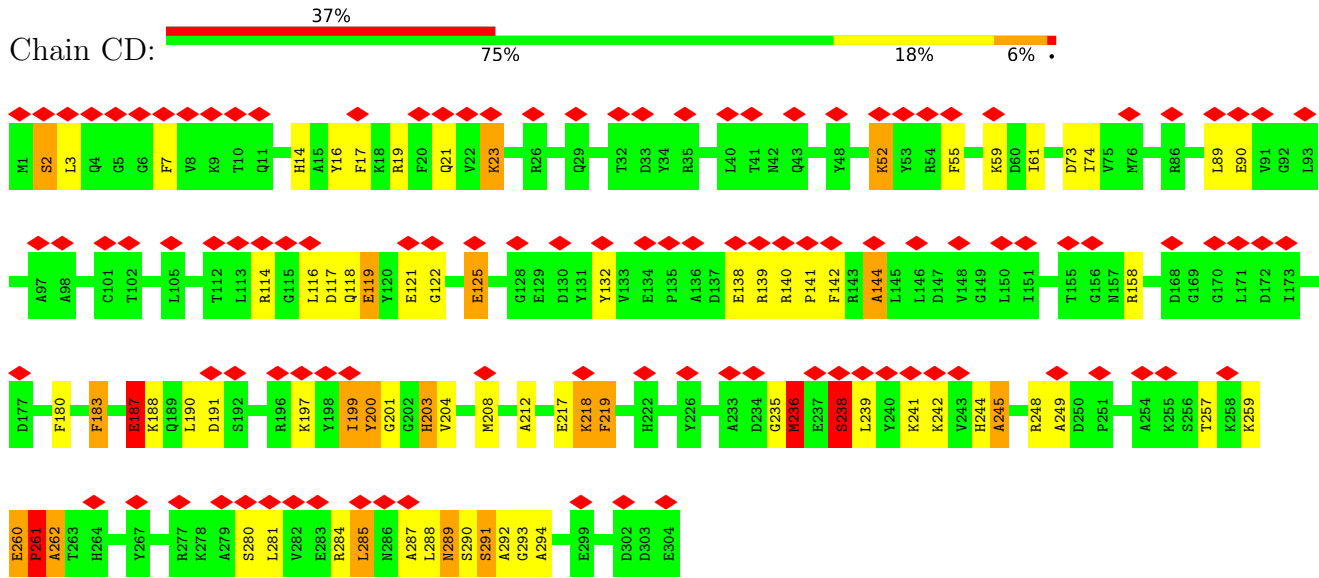
• Molecule 46: 60S ribosomal protein L15



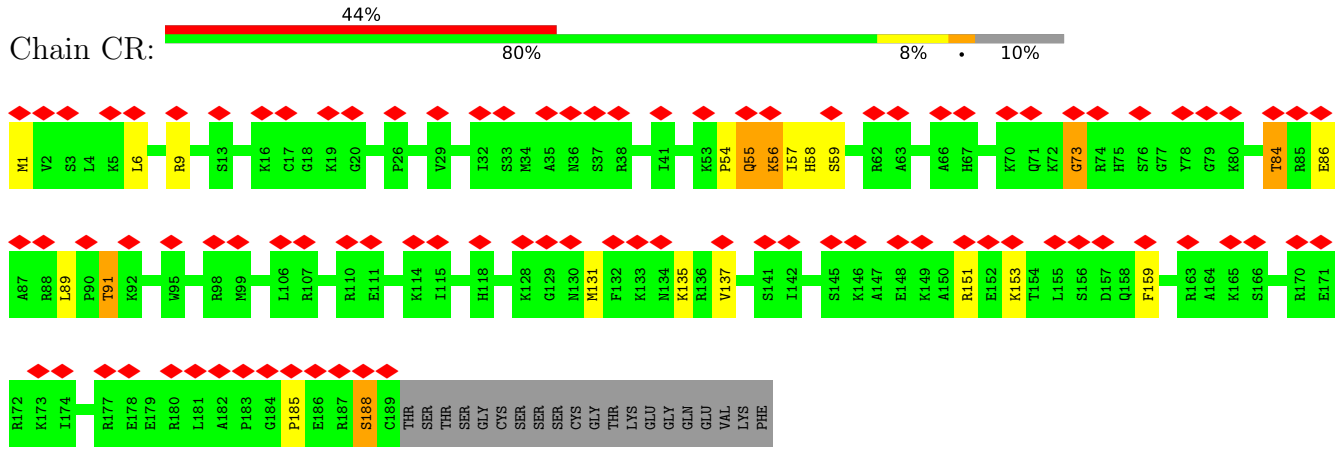
• Molecule 47: 60S ribosomal protein L18E



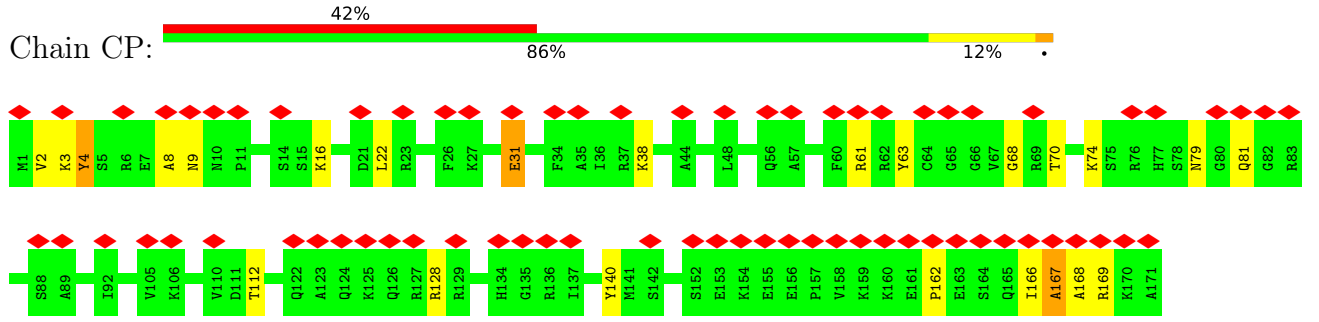
• Molecule 48: 60S ribosomal protein L18



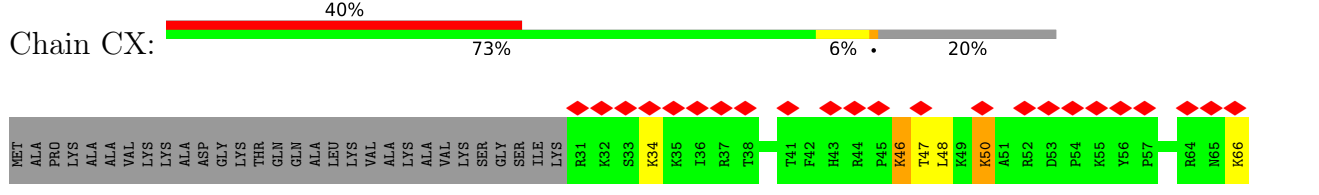
• Molecule 49: 60S ribosomal protein L19E

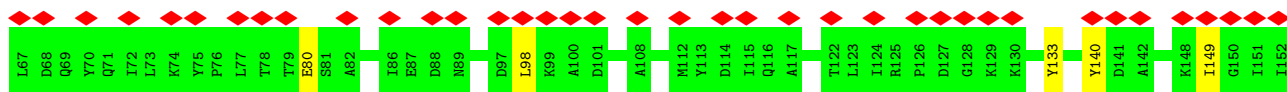


• Molecule 50: 60S ribosomal protein L22

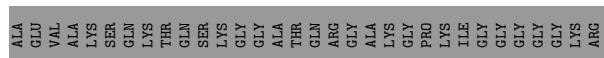
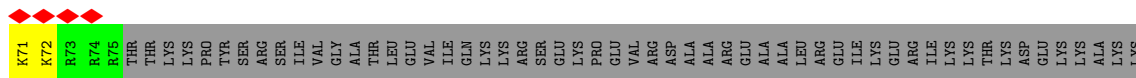
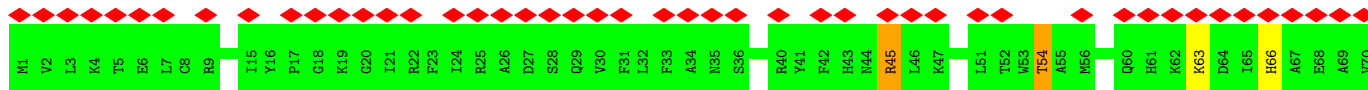


• Molecule 51: 60S ribosomal protein L23

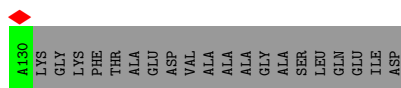
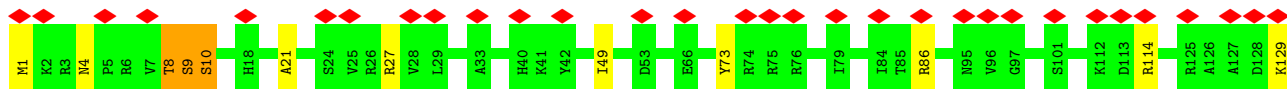
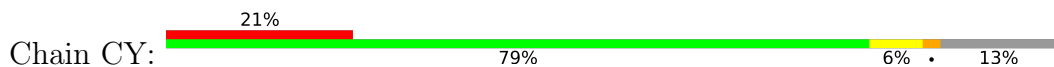




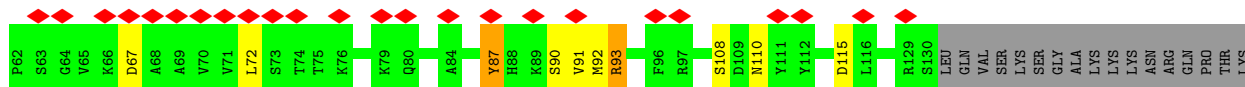
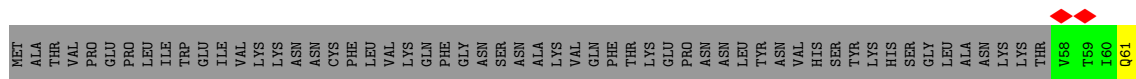
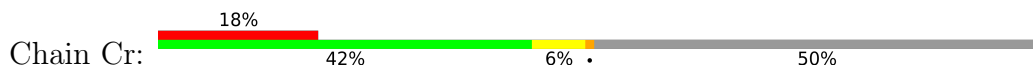
• Molecule 52: 60S ribosomal protein L24E



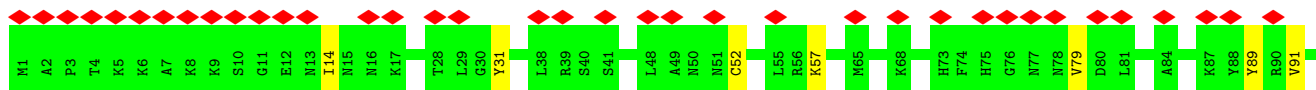
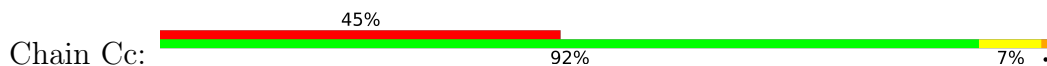
• Molecule 53: 60S ribosomal protein L24



• Molecule 54: 60S ribosomal protein L28E

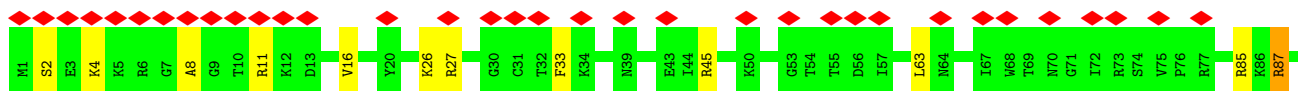
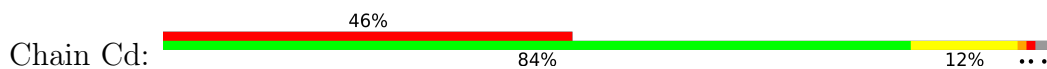


• Molecule 55: 60S ribosomal protein L30E

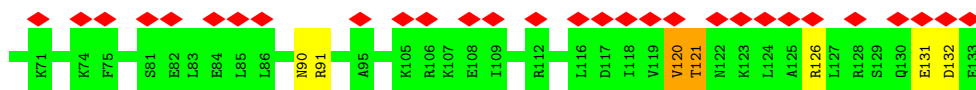
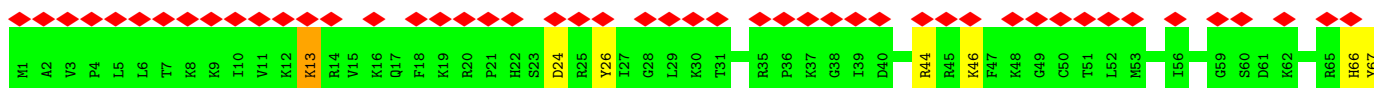
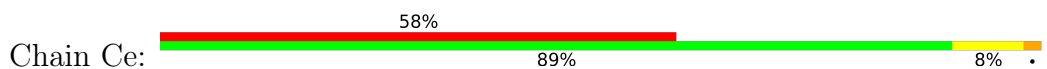




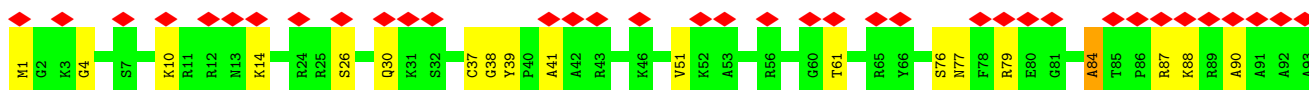
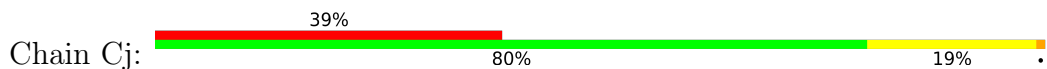
- Molecule 56: 60S ribosomal protein L31E



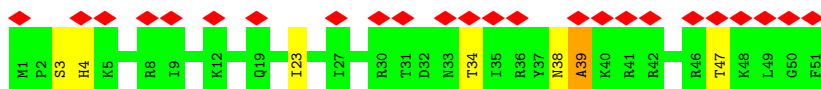
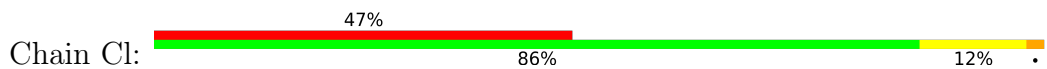
- Molecule 57: 60S ribosomal protein L32E



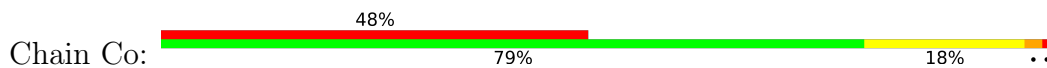
- Molecule 58: 60S ribosomal protein L37E

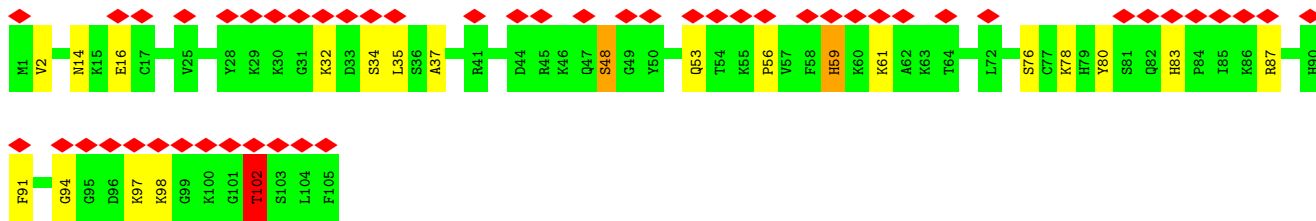


- Molecule 59: 60S ribosomal protein L39E

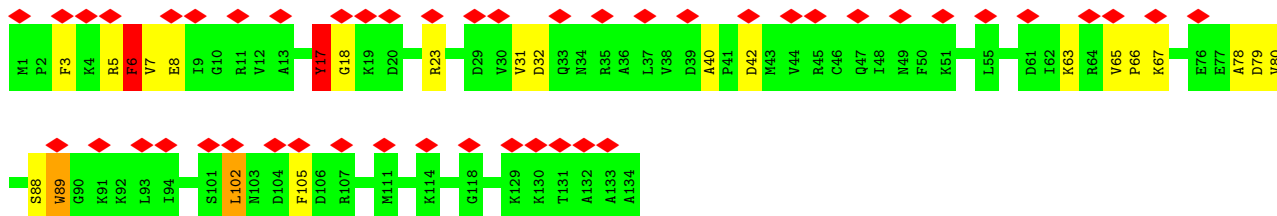
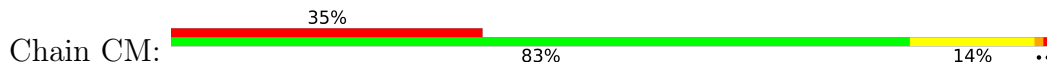


- Molecule 60: 60S ribosomal protein L44E

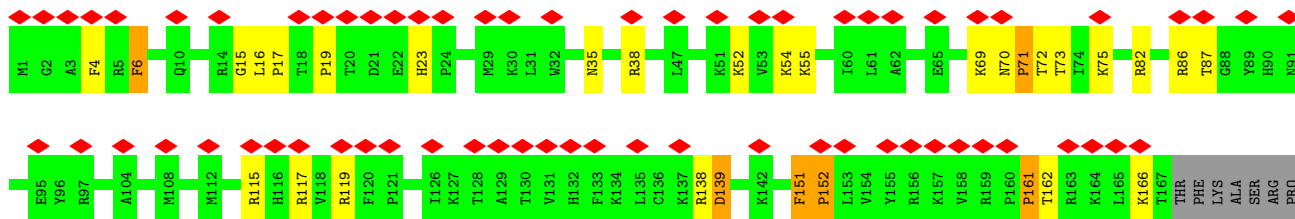
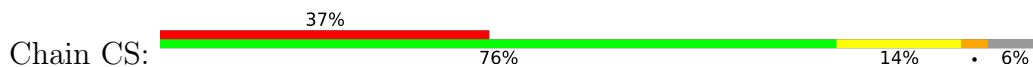




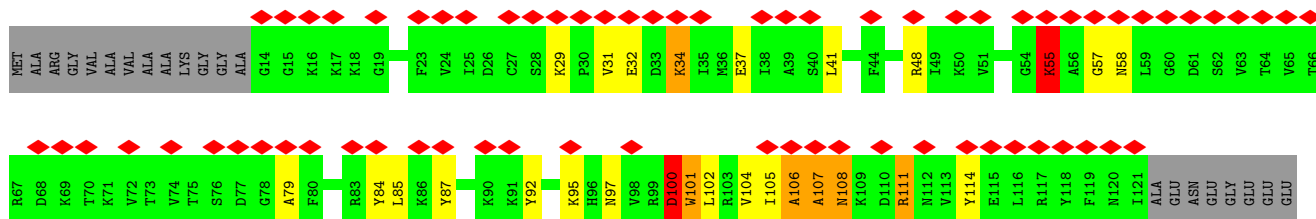
• Molecule 61: 60S ribosomal protein L14E



• Molecule 62: 60S ribosomal protein L20

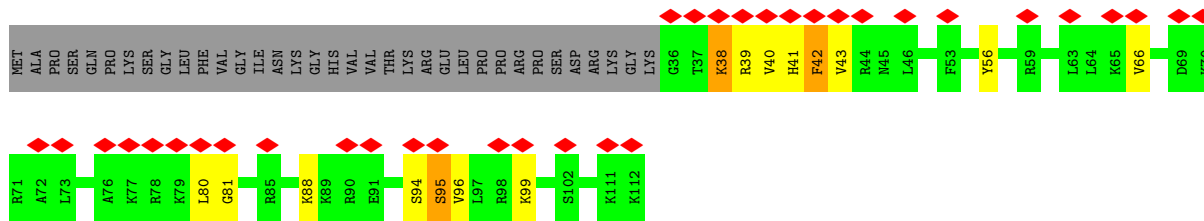


• Molecule 63: 60S ribosomal protein L22E

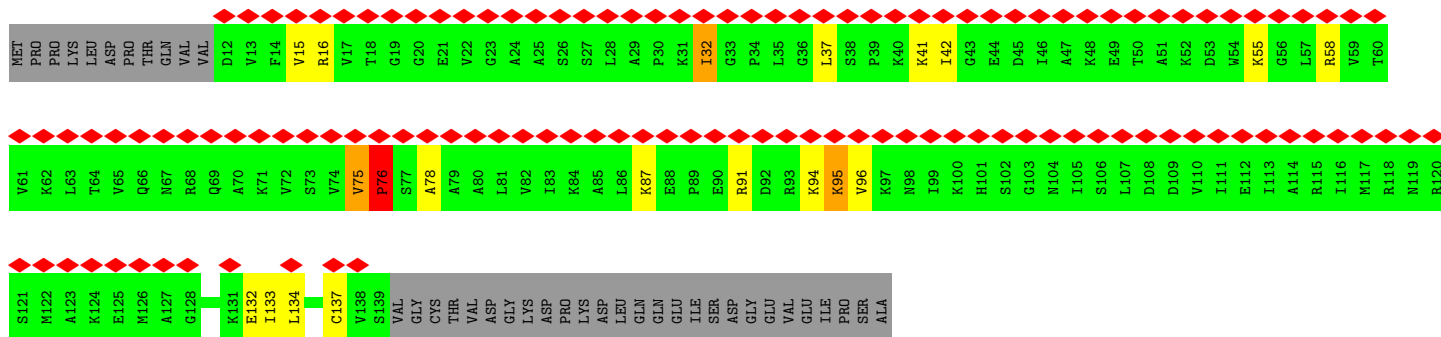
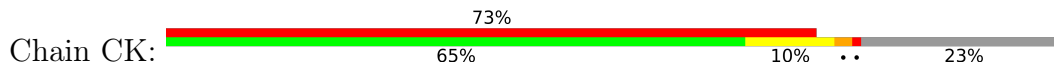


• Molecule 64: 60S ribosomal protein L36E

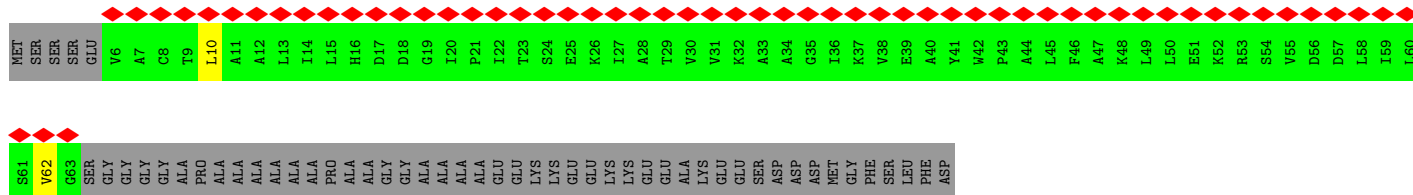




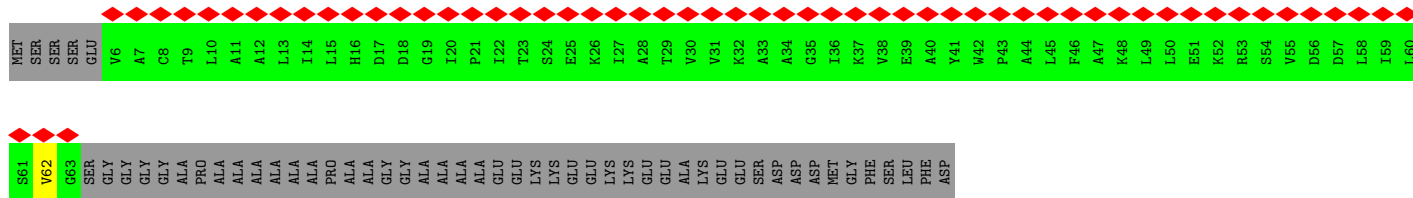
• Molecule 65: 60S ribosomal protein L11



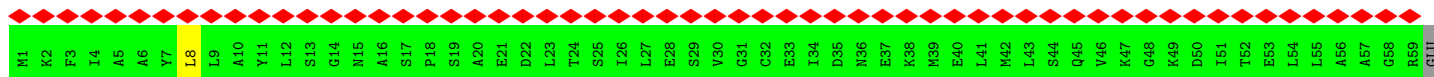
• Molecule 66: 60S ribosomal protein P1



• Molecule 66: 60S ribosomal protein P1

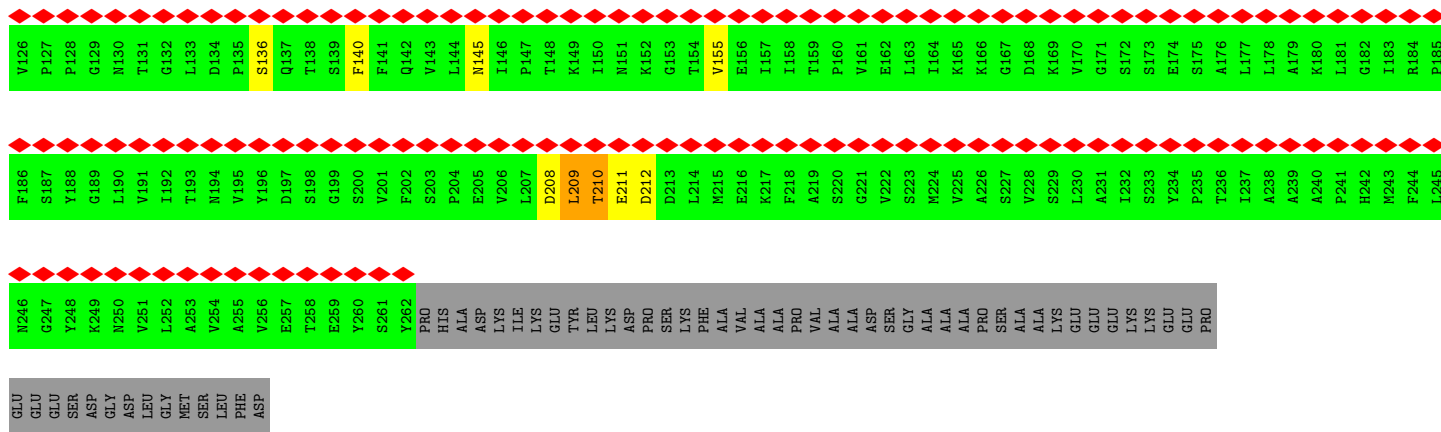


• Molecule 67: Acidic ribosomal protein P2

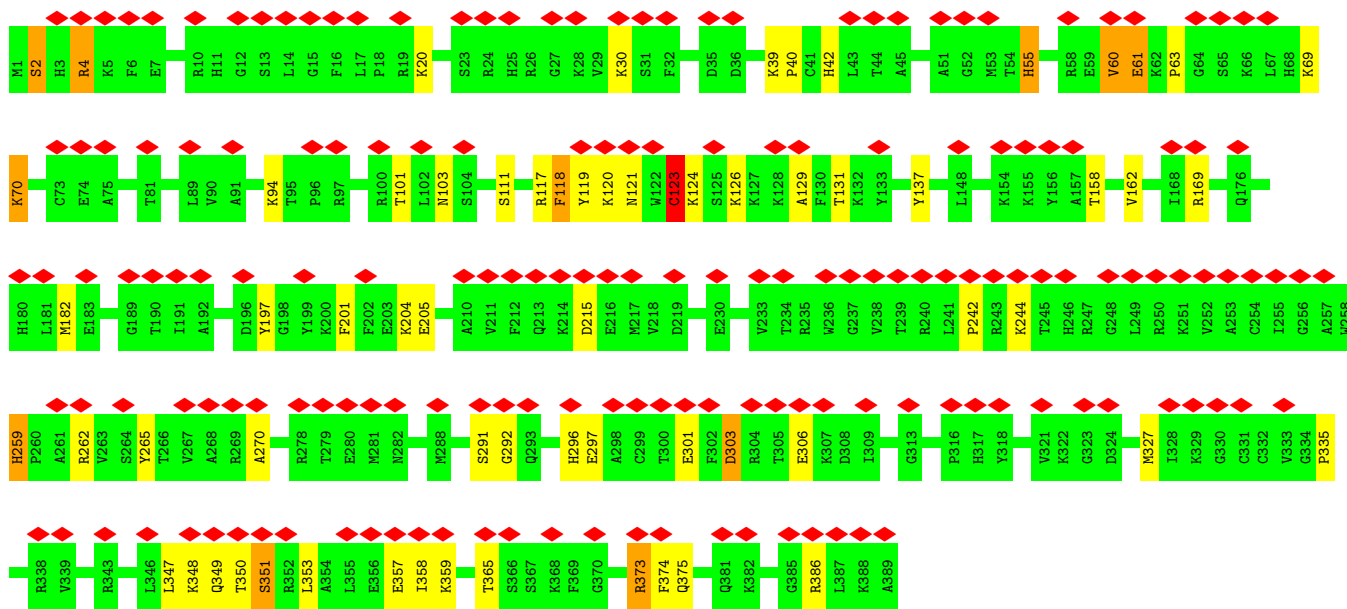
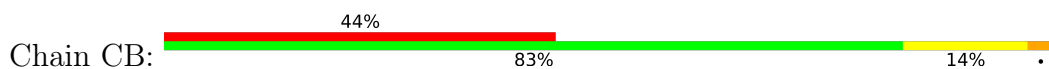




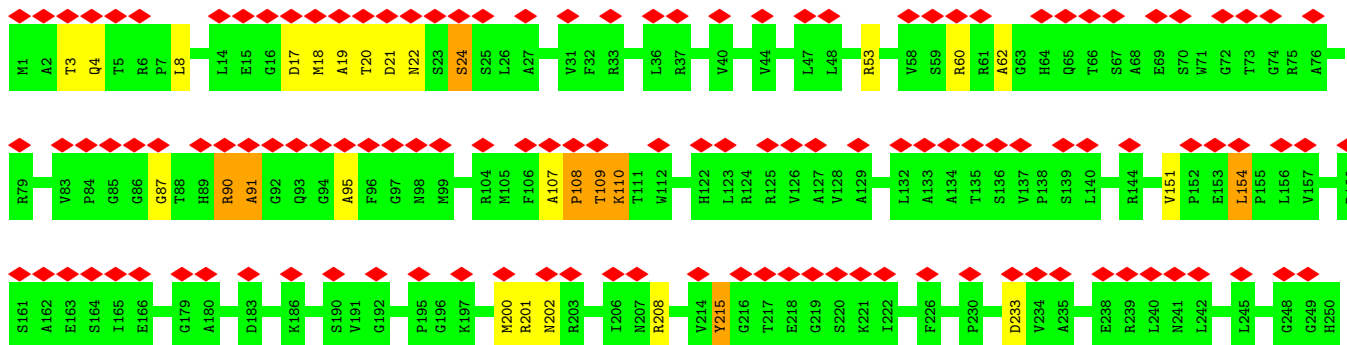
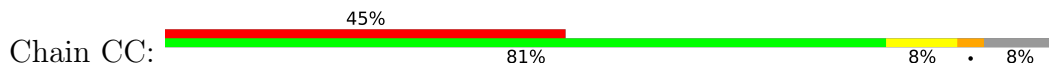


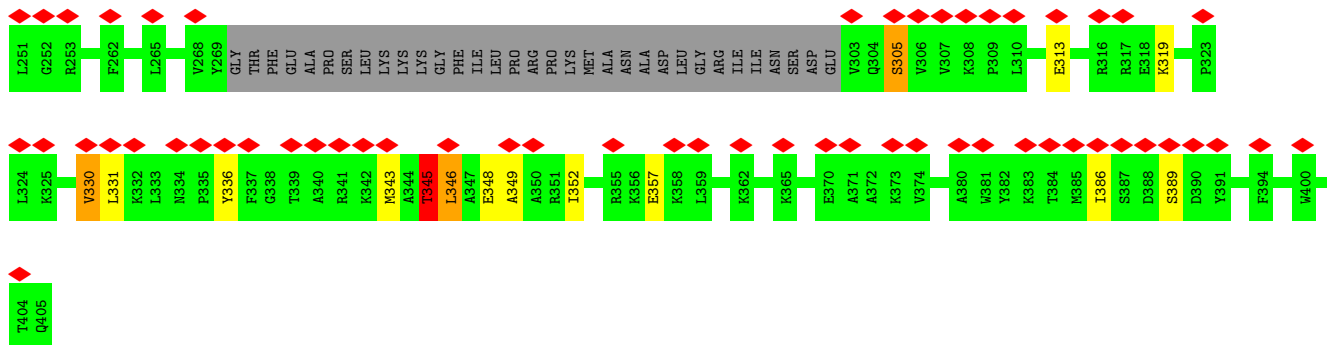


• Molecule 71: 60S ribosomal protein L3

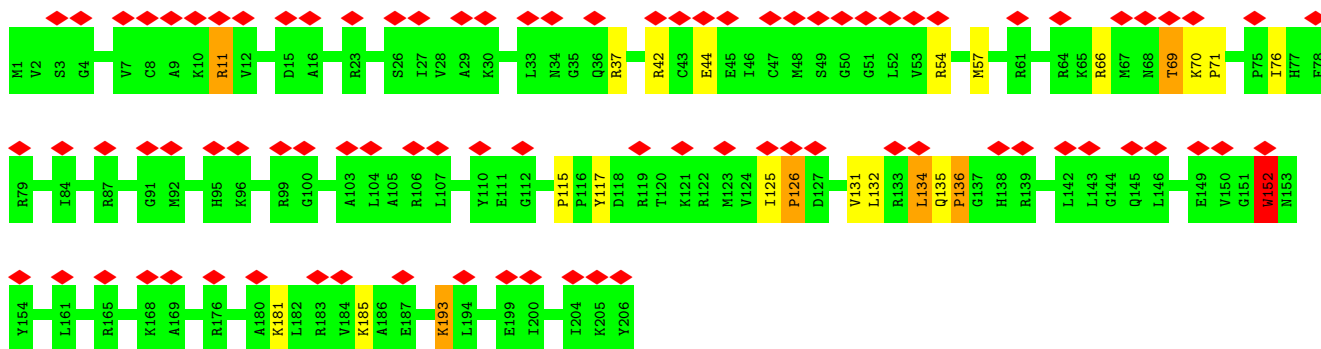
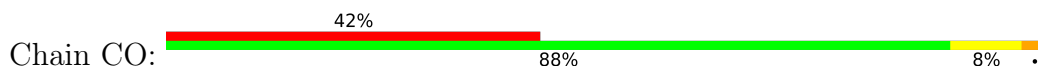


• Molecule 72: 60S ribosomal protein L4

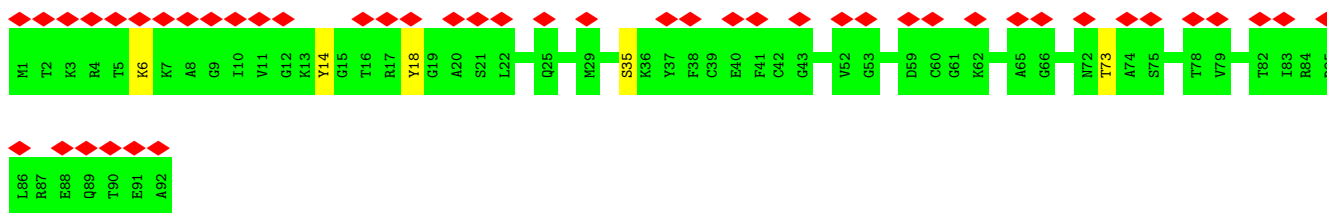




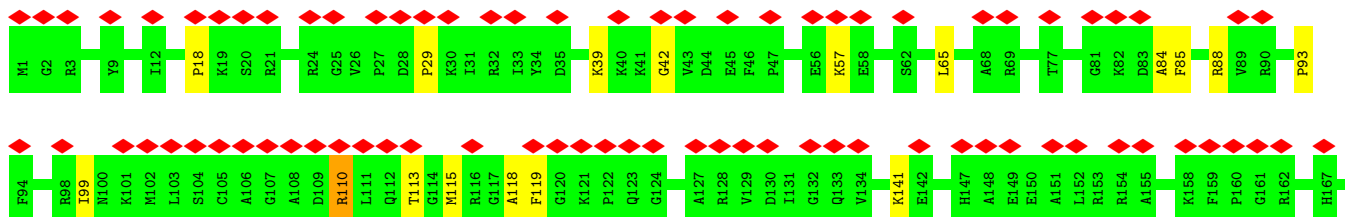
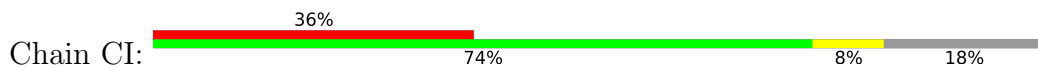
• Molecule 73: 60S ribosomal protein L13

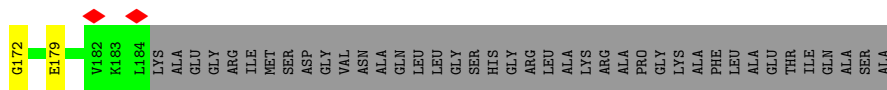


• Molecule 74: 60S ribosomal protein L43E

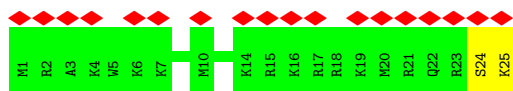
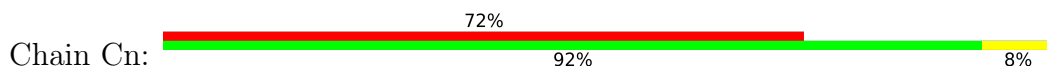


• Molecule 75: 60S ribosomal protein L16

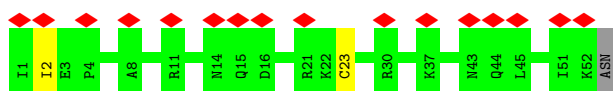




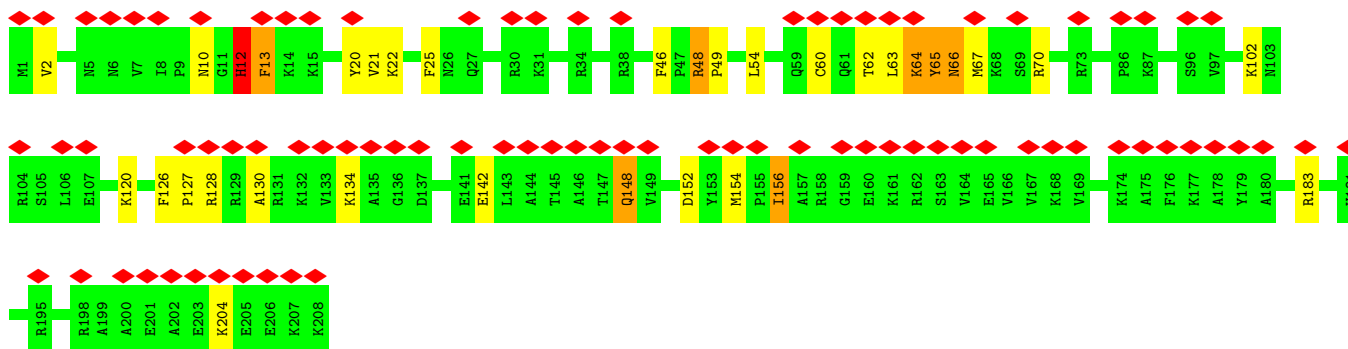
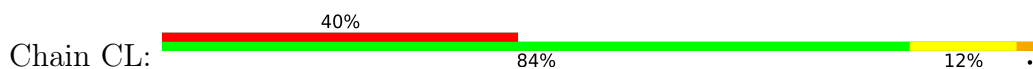
• Molecule 76: 60S ribosomal protein L41E



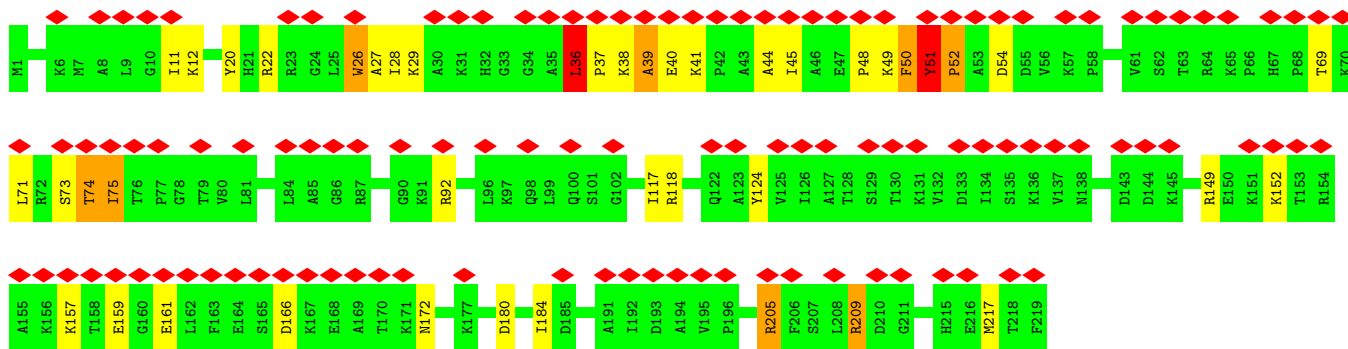
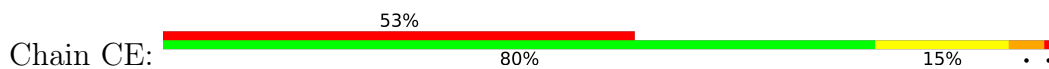
• Molecule 77: 60S ribosomal protein L40E



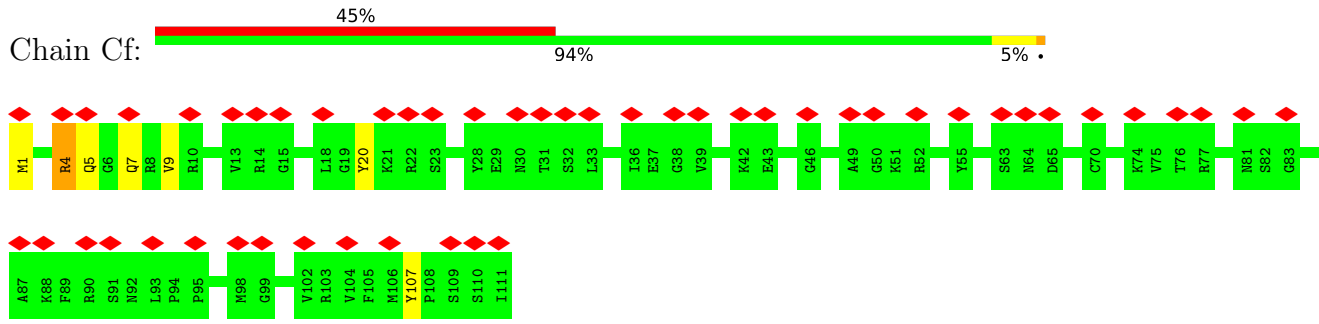
• Molecule 78: 60S ribosomal protein L13E



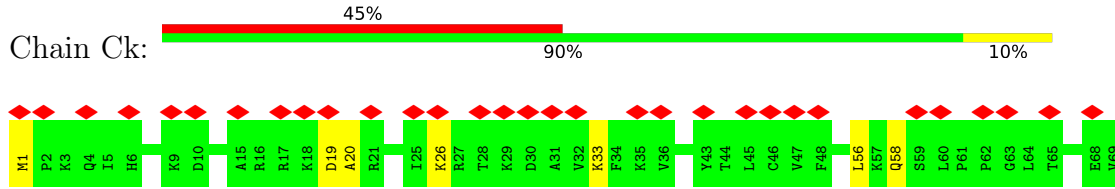
• Molecule 79: 60S ribosomal protein L6E



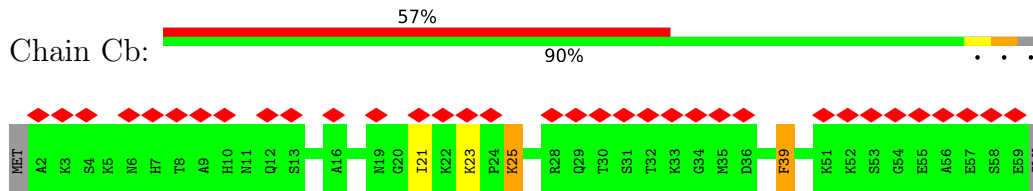
• Molecule 80: 60S ribosomal protein L33E



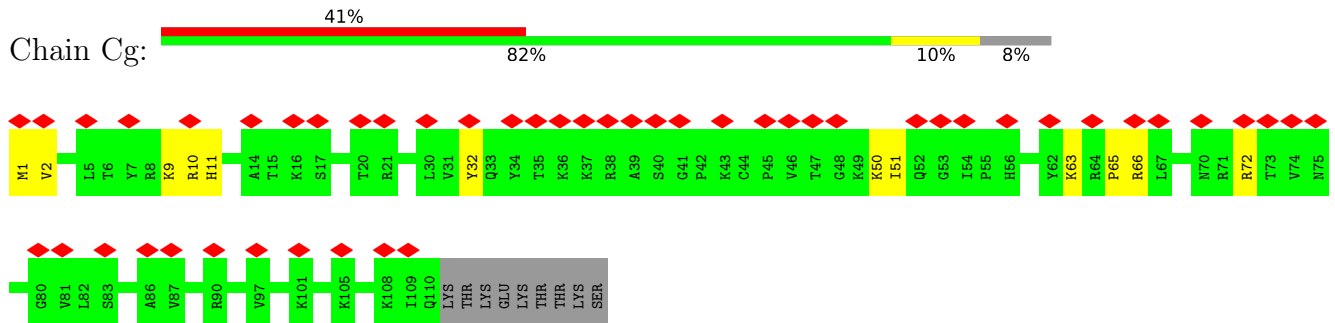
• Molecule 81: 60S ribosomal protein L38E



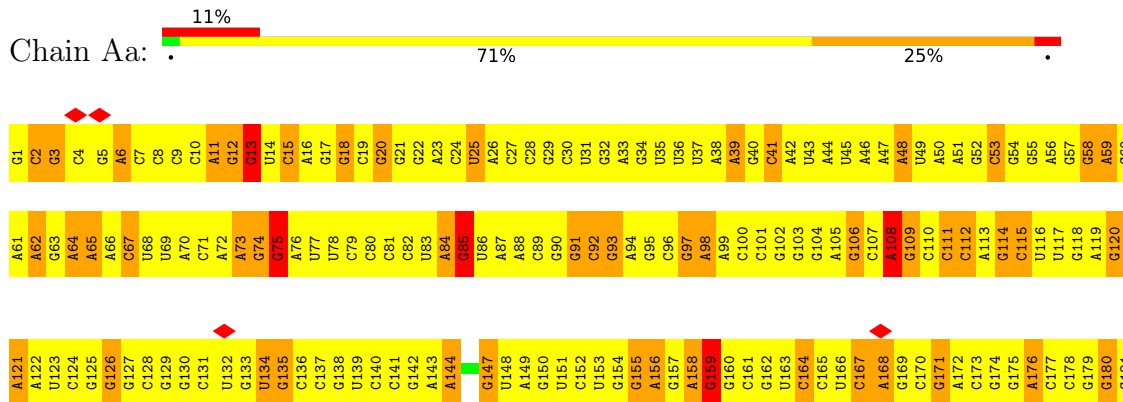
• Molecule 82: 60S ribosomal protein L29E



• Molecule 83: 60S ribosomal protein L34E



• Molecule 84: 60S ribosomal RNA



A985	A986	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	A1000	A1001	A1002	G1003	G1004	C1005	C1006	A1007	A1008	A1009	A1010	U1011	U1012	A1013	G1014	A1015	G1016	G1017	C1018	A1019	U1020	U1021	G1022	G1023	G1024																																																																															
A845	A846	G845	G846	G847	G848	A849	A850	A851	A852	A853	A854	A855	A856	A857	A858	A859	A860	A861	A862	A863	A864	A865	A866	A867	A868	A869	A870	A871	A872	A873	A874	A875	A876	A877	A878	A879	A880	A881	A882	A883	A884	A885	A886	A887	A888	A889	A890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938	A939	A940	A941	A942	A943	A944	A945	A946	A947	A948	A949	A950	A951	A952	A953	A954	A955	A956	A957	A958	A959	A960	A961	A962	A963	A964	A965	A966	A967	A968	A969	A970	A971	A972	A973	A974	A975	A976	A977	A978	A979	A980	A981	A982	A983	A984	A985	A986	A987	A988	A989	A990	A991	A992	A993	A994	A995	A996	A997	A998	A999	A1000	A1001	A1002	A1003	A1004	A1005	A1006	A1007	A1008	A1009	A1010	U1011	U1012	A1013	G1014	A1015	G1016	G1017	C1018	A1019	U1020	U1021	G1022	G1023	G1024																			
U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	U901	U902	U903	U904																																																																																	
G725	G726	G727	G728	G729	G730	G731	G732	G733	G734	G735	G736	G737	G738	G739	G740	G741	G742	G743	G744	G745	G746	G747	G748	G749	G750	G751	G752	G753	G754	G755	G756	G757	G758	G759	G760	G761	G762	G763	G764	G765	G766	G767	G768	G769	G770	G771	G772	G773	G774	G775	G776	G777	G778	G779	G780	G781	G782	G783	G784	G785	G786	G787	G788	G789	G790	G791	G792	G793	G794	G795	G796	G797	G798	G799	G800	G801	G802	G803	G804	G805	G806	G807	G808	G809	G810	G811	G812	G813	G814	G815	G816	G817	G818	G819	G820	G821	G822	G823	G824	G825	G826	G827	G828	G829	G830	G831	G832	G833	G834	G835	G836	G837	G838	G839	G840	G841	G842	G843	G844	G845	G846	G847	G848	G849	G850	G851	G852	G853	G854	G855	G856	G857	G858	G859	G860	G861	G862	G863	G864	G865	G866	G867	G868	G869	G870	G871	G872	G873	G874	G875	G876	G877	G878	G879	G880	G881	G882	G883	G884	G885	G886	G887	G888	G889	G890	G891	G892	G893	G894	G895	G896	G897	G898	G899	G900	G901	G902	G903	G904																					
G665	G666	G667	G668	G669	G670	G671	G672	G673	G674	G675	G676	G677	G678	G679	G680	G681	G682	G683	G684	G685	G686	G687	G688	G689	G690	G691	G692	G693	G694	G695	G696	G697	G698	G699	G700	G701	G702	G703	G704	G705	G706	G707	G708	G709	G710	G711	G712	G713	G714	G715	G716	G717	G718	G719	G720	G721	G722	G723	G724																																																																																																																																													
C544	C545	C546	C547	C548	C549	C550	C551	C552	C553	C554	C555	C556	C557	C558	C559	C560	C561	C562	C563	C564	C565	C566	C567	C568	C569	C570	C571	C572	C573	C574	C575	C576	C577	C578	C579	C580	C581	C582	C583	C584	C585	C586	C587	C588	C589	C590	C591	C592	C593	C594	C595	C596	C597	C598	C599	C600	C601	C602	C603	C604																																																																																																																																												
U464	U465	U466	U467	U468	U469	U470	U471	U472	U473	U474	U475	U476	U477	U478	U479	U480	U481	U482	U483	U484	U485	U486	U487	U488	U489	U490	U491	U492	U493	U494	U495	U496	U497	U498	U499	U500	U501	U502	U503	U504	U505	U506	U507	U508	U509	U510	U511	U512	U513	U514	U515	U516	U517	U518	U519	U520	U521	U522	U523	U524	U525	U526	U527	U528	U529	U530	U531	U532	U533	U534	U535	U536	U537	U538	U539	U540	U541	U542	U543	U544	U545	U546	U547	U548	U549	U550	U551	U552	U553	U554	U555	U556	U557	U558	U559	U560	U561	U562	U563	U564	U565	U566	U567	U568	U569	U570	U571	U572	U573	U574	U575	U576	U577	U578	U579	U580	U581	U582	U583	U584	U585	U586	U587	U588	U589	U590	U591	U592	U593	U594	U595	U596	U597	U598	U599	U600	U601	U602	U603	U604	U605	U606	U607	U608	U609	U610	U611	U612	U613	U614	U615	U616	U617	U618	U619	U620	U621	U622	U623	U624	U625	U626	U627	U628	U629	U630	U631	U632	U633	U634	U635	U636	U637	U638	U639	U640	U641	U642	U643	U644	U645	U646	U647	U648	U649	U650	U651	U652	U653	U654	U655	U656	U657	U658	U659	U660	U661	U662	U663	U664
G362	G363	G364	G365	G366	G367	G368	G369	G370	G371	G372	G373	G374	G375	G376	G377	G378	G379	G380	G381	G382	G383	G384	G385	G386	G387	G388	G389	G390	G391	G392	G393	G394	G395	G396	G397	G398	G399	G400	G401	G402	G403	G404	G405	G406	G407	G408	G409	G410	G411	G412	G413	G414	G415	G416	G417	G418	G419	G420	G421	G422	G423	G424	G425	G426	G427	G428	G429	G430	G431	G432	G433	G434	G435	G436	G437	G438	G439	G440	G441	G442	G443	G444	G445	G446	G447	G448	G449	G450	G451	G452	G453	G454	G455	G456	G457	G458	G459	G460	G461	G462	G463	G464	G465	G466	G467	G468	G469	G470	G471	G472	G473	G474	G475	G476	G477	G478	G479	G480	G481	G482																																																																																
U242	U243	U244	U245	U246	U247	U248	U249	U250	U251	U252	U253	U254	U255	U256	U257	U258	U259	U260	U261	U262	U263	U264	U265	U266	U267	U268	U269	U270	U271	U272	U273	U274	U275	U276	U277	U278	U279	U280	U281	U282	U283	U284	U285	U286	U287	U288	U289	U290	U291	U292	U293	U294	U295	U296	U297	U298	U299	U300	U301	U302	U303	U304	U305	U306	U307	U308	U309	U310	U311	U312	U313	U314	U315	U316	U317	U318	U319	U320	U321	U322	U323	U324	U325	U326	U327	U328	U329	U330	U331	U332	U333	U334	U335	U336	U337	U338	U339	U340	U341	U342	U343	U344	U345	U346	U347	U348	U349	U350	U351	U352	U353	U354	U355	U356	U357	U358	U359	U360	U361																																																																																	
C302	C303	C304	C305	C306	C307	C308	C309	C310	C311	C312	C313	C314	C315	C316	C317	C318	C319	C320	C321	C322	C323	C324	C325	C326	C327	C328	C329	C330	C331	C332	C333	C334	C335	C336	C337	C338	C339	C340	C341	C342	C343	C344	C345	C346	C347	C348	C349	C350	C351	C352	C353	C354	C355	C356	C357	C358	C359	C360	C361	C362	C363	C364	C365	C366	C367	C368	C369	C370	C371	C372	C373	C374	C375	C376	C377	C378	C379	C380	C381	C382	C383	C384	C385	C386	C387	C388	C389	C390	C391	C392	C393	C394	C395	C396	C397	C398	C399	C400	C401	C402	C403	C404	C405	C406	C407	C408	C409	C410	C411	C412	C413	C414	C415	C416	C417	C418	C419	C420	C421	C422	C423	C424	C425	C426	C427	C428	C429	C430	C431	C432	C433	C434	C435	C436	C437	C438	C439	C440	C441	C442	C443	C444	C445	C446	C447	C448	C449	C450	C451	C452	C453	C454	C455	C456	C457	C458	C459	C460	C461	C462	C463	C464	C465	C466	C467	C468	C469	C470	C471	C472	C473	C474	C475	C476	C477	C478	C479	C480	C481	C482																				
C182	C183	C184	C185	C186	C187	C188	C189	C190	C191	C192	C193	C194	C195	C196	C197	C198	C199	C200	C201	C202	C203	C204	C205	C206	C207	C208	C209	C210	C211	C212	C213	C214	C215	C216	C217	C218	C219	C220	C221	C222	C223	C224	C225	C226	C227	C228	C229	C230	C231	C232	C233	C234	C235	C236	C237	C238	C239	C240	C241																																																																																																																																													

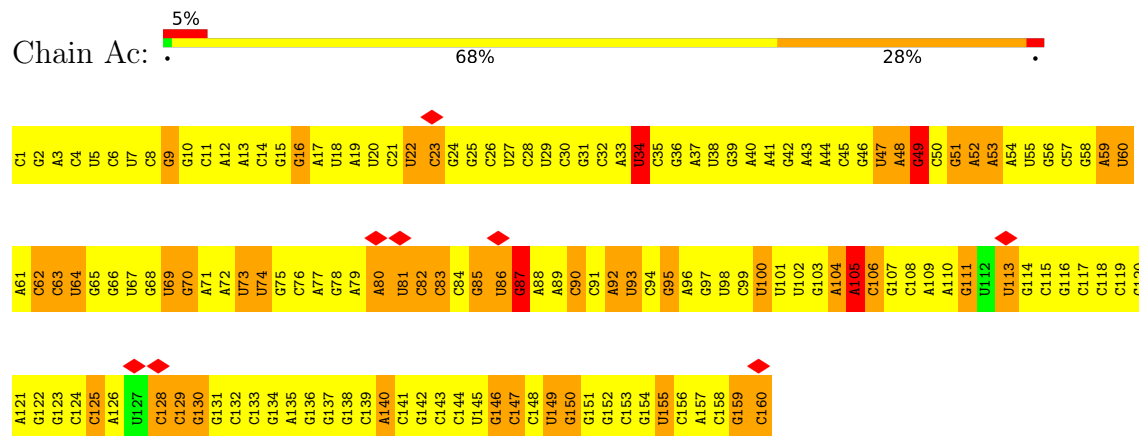
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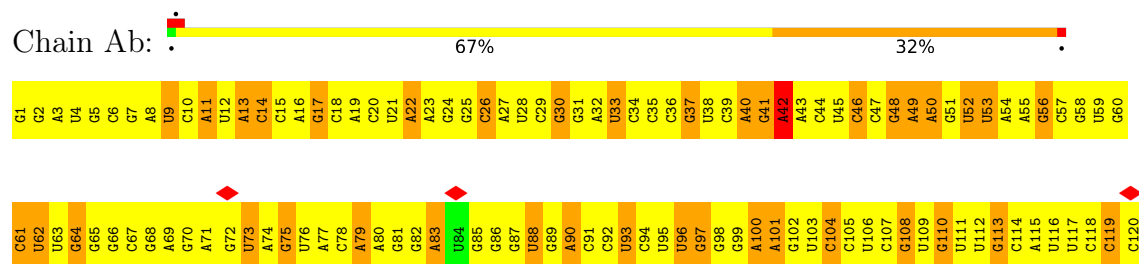
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C3247	C3248	C3249	C3250	C3251	C3252	C3253	C3254	C3255	C3256	C3257	C3258	C3259	C3260	C3261	C3262	C3263	C3264	C3265	C3266	C3267	C3268	C3269	C3270	C3271	C3272	C3273	C3274	C3275	C3276	C3277	C3278	C3279	C3280	C3281	C3282	C3283	C3284	C3285	C3286	C3287	C3288	C3289	C3290	C3291	C3292	C3293	C3294	C3295	C3296	C3297	C3298	C3299	C3300	C3301	C3302	C3303	C3304	C3305	A3306		
C3187	C3188	C3189	U3190	U3191	C3192	C3193	C3194	C3195	C3196	C3197	C3198	C3199	A3200	A3201	C3202	C3203	C3204	C3205	C3206	C3207	C3208	C3209	C3210	C3211	C3212	C3213	C3214	C3215	C3216	C3217	C3218	C3219	A3220	A3221	C3222	C3223	C3224	C3225	C3226	U3227	C3228	C3229	C3230	C3231	C3232	C3233	C3234	A3235	C3236	C3237	U3238	C3239	C3240	C3241	C3242	C3243	C3244	U3245			
C3127	A3128	C3129	A3130	U3131	C3132	C3133	C3134	A3135	C3136	C3137	C3138	C3139	A3140	C3141	C3142	C3143	C3144	C3145	C3146	C3147	C3148	C3149	C3150	C3151	C3152	C3153	C3154	C3155	C3156	C3157	C3158	C3159	C3160	C3161	C3162	C3163	C3164	C3165	C3166	C3167	C3168	C3169	C3170	C3171	C3172	C3173	C3174	C3175	C3176	C3177	C3178	C3179	U3180	U3181	C3182	C3183	C3184	C3185	C3186		
C3067	U3068	U3069	C3070	A3071	A3072	A3073	A3074	A3075	C3076	C3077	C3078	C3079	U3080	C3081	C3082	C3083	C3084	C3085	C3086	C3087	A3088	A3089	C3090	C3091	A3092	C3093	C3094	C3095	C3096	C3097	U3098	C3099	C3100	C3101	C3102	C3103	A3104	U3105	U3106	A3107	U3108	C3109	A3110	C3111	U3112	C3113	A3114	A3115	C3116	C3117	C3118	C3119	U3120	C3121	U3122	A3123	C3124	C3125	U3126		
G2947	A2948	G2949	C2950	U2951	C2952	C2953	G2954	C2955	U2956	C2957	A2958	C2959	A2960	C2961	C2962	C2963	U2964	C2965	C2966	U2967	C2968	C2969	C2970	A2971	C2972	A2973	C2974	C2975	U2976	U2977	A2978	C2979	U2980	U2981	U2982	U2983	A2984	C2985	C2986	C2987	C2988	C2989	C2990	U2991	C2992	C2993	C2994	U2995	C2996	C2997	A2998	C2999	U3000	G3001	C3002	C3003	C3004	C3005	C3006		
G2827	U2828	U2829	G2830	U2831	C2832	C2833	C2834	A2835	C2836	C2837	C2838	A2839	A2840	G2841	C2842	C2843	U2844	U2845	C2846	A2847	U2848	A2849	C2850	C2851	C2852	A2853	C2854	C2855	C2856	U2857	C2858	C2859	U2860	U2861	U2862	U2863	U2864	C2865	C2866	U2867	C2868	C2869	U2870	C2871	C2872	C2873	A2874	C2875	C2876	C2877	C2878	C2879	C2880	C2881	C2882	C2883	C2884	U2885	C2886		
C2887	U2888	U2889	U2890	C2891	C2892	U2893	U2894	C2895	C2896	C2897	A2898	C2899	C2900	C2901	A3022	C3023	U3024	A3025	C3026	U3027	C3028	C3029	C3030	C3031	C3032	C3033	A3034	C3035	C3036	U3037	U3038	U3039	C3040	A3041	U3042	U3043	C3044	A3045	C3046	C3047	C3048	A3049	C3050	U3051	C3052	C3053	C3054	U3055	C3056	A3057	U3058	C3059	C3060	C3061	C3062	C3063	C3064	C3065	U3066	U3067	C3068
G2767	C2768	U2769	C2770	U2771	A2772	C2773	A2774	C2775	U2776	U2777	C2778	C2779	U2791	A2792	C2793	C2794	C2795	C2796	U2797	C2798	U2799	C2800	A2801	C2802	A2803	A2804	A2805	A2806	C2807	C2808	U2809	A2810	C2811	C2812	A2813	C2814	U2815	C2816	C2817	C2818	A2819	U2820	C2821	C2822	C2823	U2824	C2825	C2826													
C2647	C2648	C2649	A2650	C2651	C2652	U2653	C2654	U2655	C2656	C2657	U2658	A2659	U2660	C2661	A2662	U2663	C2664	A2665	C2666	U2667	U2668	C2669	A2670	C2671	C2672	C2673	C2674	C2675	C2676	C2677	C2678	C2679	C2680	A2681	C2682	A2683	U2684	C2685	C2686	C2687	C2688	U2689	A2690	C2691	C2692	C2693	U2694	C2695	C2696	A2697	C2698	A2699	U2700	C2701	C2702	C2703	U2704	A2705	A2706		
A2707	A2708	C2709	C2710	U2711	C2712	C2713	U2714	U2715	U2716	C2717	U2718	U2719	U2720	C2721	U2722	C2723	U2724	U2725	U2726	U2727	C2728	C2729	A2730	C2731	U2732	A2733	C2734	C2735	C2736	U2737	U2738	U2739	C2740	C2741	A2742	A2743	C2744	C2745	C2746	U2747	C2748	U2749	A2750	C2751	C2752	C2753	C2754	U2755	C2756	C2757	C2758	C2759	U2760	U2761	C2762	C2763	C2764	U2765	U2766		



• Molecule 85: 5.8S ribosomal RNA



• Molecule 86: 5S ribosomal RNA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	2108230	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Wiener Filter on 3D volumes (SPIDER)	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	38900	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.454	Depositor
Minimum map value	-0.200	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.11	Depositor
Map size ( $\text{\AA}$ )	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ( $^\circ$ )	90, 90, 90	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.2375, 1.2375, 1.2375	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	Ad	2.49	2030/42036 (4.8%)	2.11	2382/65520 (3.6%)
2	Ae	2.62	95/1781 (5.3%)	2.13	105/2775 (3.8%)
3	Af	2.45	12/260 (4.6%)	2.06	16/403 (4.0%)
4	BY	0.99	0/1123	1.10	1/1487 (0.1%)
5	BI	1.05	0/539	0.95	0/712
6	BK	0.93	0/840	1.21	6/1135 (0.5%)
7	BM	0.82	0/936	1.11	2/1260 (0.2%)
8	Bf	0.93	0/590	1.17	1/788 (0.1%)
9	BX	0.96	0/1122	1.05	4/1492 (0.3%)
10	Bg	0.97	0/2988	1.06	3/4049 (0.1%)
11	BD	1.01	0/1652	1.20	4/2222 (0.2%)
12	BE	0.99	0/1637	1.07	0/2202
13	BF	0.98	0/1509	1.00	3/2034 (0.1%)
14	BQ	1.11	0/1034	1.19	6/1379 (0.4%)
15	BU	0.93	0/995	1.14	3/1338 (0.2%)
16	BO	1.05	0/909	1.11	2/1217 (0.2%)
17	BS	1.04	0/1258	1.15	5/1674 (0.3%)
18	BN	0.96	0/994	1.13	5/1332 (0.4%)
19	BL	1.04	0/704	1.15	3/944 (0.3%)
20	BT	1.01	0/1179	1.08	3/1586 (0.2%)
21	BP	0.91	0/727	1.11	2/975 (0.2%)
22	BZ	0.94	0/791	1.18	7/1057 (0.7%)
23	Bc	1.04	0/455	1.26	2/609 (0.3%)
24	BW	1.02	0/1060	1.16	6/1419 (0.4%)
25	Bd	1.11	0/386	1.25	4/510 (0.8%)
26	Bb	0.92	0/674	1.04	0/905
27	Be	1.07	0/476	1.01	0/627
28	BA	0.96	0/1567	1.06	4/2121 (0.2%)
29	BR	1.03	0/955	1.03	1/1273 (0.1%)
30	BB	0.96	0/1736	1.12	4/2329 (0.2%)
31	BV	1.00	0/610	1.07	0/820
32	Ba	1.07	0/766	1.13	0/1023
33	BJ	1.09	0/1553	1.05	4/2079 (0.2%)
34	BC	0.93	0/1701	1.05	3/2298 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	BG	1.06	0/1888	1.05	4/2507 (0.2%)
36	BH	3.40	1/1535 (0.1%)	1.14	4/2065 (0.2%)
37	CG	0.94	0/1939	1.01	5/2598 (0.2%)
38	CT	0.99	0/1316	1.11	2/1772 (0.1%)
39	CZ	1.00	0/1110	1.02	2/1480 (0.1%)
40	Cz	0.89	0/1741	1.00	1/2323 (0.0%)
41	CA	1.05	0/1992	1.15	10/2681 (0.4%)
42	CJ	1.06	0/1401	1.14	7/1869 (0.4%)
43	CH	0.96	0/1519	1.03	0/2042
44	CV	0.99	0/1064	1.07	0/1425
45	CN	1.12	0/1669	1.07	6/2235 (0.3%)
46	Ca	0.98	0/1143	1.17	4/1527 (0.3%)
47	CQ	1.04	0/1303	1.11	5/1748 (0.3%)
48	CD	1.00	0/2489	1.23	22/3342 (0.7%)
49	CR	1.09	0/1590	1.06	4/2100 (0.2%)
50	CP	1.03	0/1397	1.14	6/1871 (0.3%)
51	CX	0.90	0/1002	1.03	3/1340 (0.2%)
52	CW	1.04	0/649	1.07	1/861 (0.1%)
53	CY	1.10	0/1061	1.08	4/1418 (0.3%)
54	Cr	0.98	0/585	1.16	1/786 (0.1%)
55	Cc	0.86	0/869	0.98	1/1169 (0.1%)
56	Cd	1.01	0/970	1.10	4/1295 (0.3%)
57	Ce	1.01	0/1122	1.06	4/1497 (0.3%)
58	Cj	1.17	0/769	1.16	1/1019 (0.1%)
59	Cl	1.14	0/472	1.12	1/627 (0.2%)
60	Co	0.93	0/867	1.12	3/1144 (0.3%)
61	CM	0.99	0/1094	1.10	4/1461 (0.3%)
62	CS	1.01	0/1457	1.16	3/1957 (0.2%)
63	CU	0.98	0/876	1.27	12/1170 (1.0%)
64	Ci	1.07	0/618	1.16	5/809 (0.6%)
65	CK	0.92	0/968	1.11	1/1299 (0.1%)
66	Cu	0.78	0/438	0.91	0/596
66	Cv	0.79	0/438	0.90	0/596
67	Cs	0.83	0/444	0.82	0/596
67	Ct	0.84	0/444	0.81	0/596
68	Ch	1.02	0/1023	1.05	2/1359 (0.1%)
69	CF	0.98	0/2020	1.00	4/2708 (0.1%)
70	Cq	0.87	0/2023	0.96	5/2739 (0.2%)
71	CB	0.97	0/3207	1.14	16/4289 (0.4%)
72	CC	1.01	0/2951	1.11	8/3972 (0.2%)
73	CO	1.03	0/1678	1.07	6/2246 (0.3%)
74	Cp	1.00	0/724	1.02	1/958 (0.1%)
75	CI	1.01	0/1523	1.00	1/2036 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Cn	1.34	0/239	1.04	0/302
77	Cm	1.01	0/434	0.95	0/574
78	CL	1.03	0/1721	1.13	6/2299 (0.3%)
79	CE	0.95	0/1766	1.16	8/2374 (0.3%)
80	Cf	1.05	0/908	1.13	3/1215 (0.2%)
81	Ck	0.98	0/572	1.09	0/763
82	Cb	0.98	0/486	1.06	2/641 (0.3%)
83	Cg	1.07	0/913	1.02	0/1223
84	Aa	1.61	170/81235 (0.2%)	2.52	9121/126706 (7.2%)
85	Ac	1.61	7/3809 (0.2%)	2.48	426/5936 (7.2%)
86	Ab	2.31	125/2864 (4.4%)	2.91	380/4464 (8.5%)
All	All	1.65	2440/227878 (1.1%)	2.00	12710/334219 (3.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	BY	0	1
6	BK	0	4
7	BM	0	1
8	Bf	0	1
10	Bg	0	1
11	BD	0	3
12	BE	0	2
13	BF	0	2
14	BQ	0	1
15	BU	0	2
17	BS	0	1
19	BL	0	1
20	BT	0	4
23	Bc	0	1
24	BW	0	1
25	Bd	0	1
26	Bb	0	2
29	BR	0	1
30	BB	0	1
32	Ba	0	1
35	BG	0	1
36	BH	0	4
37	CG	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
41	CA	0	4
42	CJ	0	2
43	CH	0	3
45	CN	0	1
46	Ca	0	7
47	CQ	0	6
48	CD	0	13
49	CR	0	3
50	CP	0	1
51	CX	0	1
55	Cc	0	1
57	Ce	0	1
58	Cj	0	1
59	Cl	0	1
60	Co	0	2
61	CM	0	4
62	CS	0	3
63	CU	0	2
65	CK	0	2
68	Ch	0	1
69	CF	0	3
70	Cq	0	2
71	CB	0	9
72	CC	0	4
73	CO	0	4
74	Cp	0	1
75	CI	0	4
78	CL	0	5
79	CE	0	7
80	Cf	0	2
83	Cg	0	1
84	Aa	0	309
85	Ac	0	18
86	Ab	0	19
All	All	0	486

The worst 5 of 2440 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	BH	117	ARG	CZ-NH2	127.06	2.98	1.33
1	Ad	1203	G	C2'-C1'	23.55	1.79	1.53
2	Ae	28	G	C2'-C1'	-23.31	1.27	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Ad	218	G	C2'-C1'	-23.01	1.28	1.53
1	Ad	999	G	C2'-C1'	-22.88	1.28	1.53

The worst 5 of 12710 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ad	1005	C	O4'-C1'-N1	31.46	133.37	108.20
1	Ad	1462	C	O4'-C1'-N1	29.23	131.58	108.20
1	Ad	547	C	O4'-C1'-N1	28.96	131.37	108.20
1	Ad	1765	A	O4'-C1'-N9	28.77	131.22	108.20
84	Aa	2162	C	P-O3'-C3'	27.64	152.86	119.70

There are no chirality outliers.

5 of 486 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	BK	22	TYR	Sidechain
6	BK	83	PRO	Peptide
6	BK	86	ILE	Peptide
6	BK	87	VAL	Peptide
4	BY	48	LYS	Peptide

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	BY	136/138 (99%)	118 (87%)	8 (6%)	10 (7%)	1	13
5	BI	64/220 (29%)	61 (95%)	2 (3%)	1 (2%)	9	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	BK	94/183 (51%)	66 (70%)	17 (18%)	11 (12%)	0	6
7	BM	121/171 (71%)	84 (69%)	20 (16%)	17 (14%)	0	4
8	Bf	69/155 (44%)	46 (67%)	10 (14%)	13 (19%)	0	2
9	BX	140/142 (99%)	124 (89%)	11 (8%)	5 (4%)	3	25
10	Bg	378/380 (100%)	334 (88%)	26 (7%)	18 (5%)	2	21
11	BD	206/208 (99%)	125 (61%)	34 (16%)	47 (23%)	0	1
12	BE	198/265 (75%)	173 (87%)	16 (8%)	9 (4%)	2	22
13	BF	189/191 (99%)	162 (86%)	20 (11%)	7 (4%)	3	25
14	BQ	124/149 (83%)	93 (75%)	15 (12%)	16 (13%)	0	5
15	BU	126/128 (98%)	102 (81%)	14 (11%)	10 (8%)	1	12
16	BO	117/151 (78%)	91 (78%)	12 (10%)	14 (12%)	0	6
17	BS	150/152 (99%)	109 (73%)	16 (11%)	25 (17%)	0	3
18	BN	119/151 (79%)	92 (77%)	14 (12%)	13 (11%)	0	8
19	BL	83/160 (52%)	61 (74%)	16 (19%)	6 (7%)	1	14
20	BT	144/146 (99%)	123 (85%)	13 (9%)	8 (6%)	2	18
21	BP	89/154 (58%)	69 (78%)	12 (14%)	8 (9%)	1	11
22	BZ	98/108 (91%)	75 (76%)	10 (10%)	13 (13%)	0	4
23	Bc	56/65 (86%)	40 (71%)	5 (9%)	11 (20%)	0	2
24	BW	128/130 (98%)	101 (79%)	16 (12%)	11 (9%)	1	11
25	Bd	46/56 (82%)	29 (63%)	6 (13%)	11 (24%)	0	1
26	Bb	84/86 (98%)	75 (89%)	6 (7%)	3 (4%)	3	25
27	Be	58/62 (94%)	49 (84%)	5 (9%)	4 (7%)	1	14
28	BA	195/260 (75%)	176 (90%)	10 (5%)	9 (5%)	2	21
29	BR	114/141 (81%)	89 (78%)	15 (13%)	10 (9%)	1	11
30	BB	209/262 (80%)	153 (73%)	31 (15%)	25 (12%)	0	6
31	BV	74/82 (90%)	62 (84%)	9 (12%)	3 (4%)	3	22
32	Ba	91/133 (68%)	65 (71%)	13 (14%)	13 (14%)	0	4
33	BJ	185/195 (95%)	162 (88%)	16 (9%)	7 (4%)	3	24
34	BC	212/263 (81%)	189 (89%)	16 (8%)	7 (3%)	4	26
35	BG	227/245 (93%)	211 (93%)	10 (4%)	6 (3%)	5	31
36	BH	182/189 (96%)	154 (85%)	10 (6%)	18 (10%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	CG	235/257 (91%)	205 (87%)	24 (10%)	6 (3%)	5	31
38	CT	158/164 (96%)	137 (87%)	6 (4%)	15 (10%)	0	10
39	CZ	134/136 (98%)	123 (92%)	10 (8%)	1 (1%)	22	62
40	Cz	214/216 (99%)	197 (92%)	9 (4%)	8 (4%)	3	25
41	CA	253/261 (97%)	219 (87%)	19 (8%)	15 (6%)	1	17
42	CJ	168/180 (93%)	132 (79%)	14 (8%)	22 (13%)	0	4
43	CH	188/190 (99%)	167 (89%)	16 (8%)	5 (3%)	5	31
44	CV	138/140 (99%)	124 (90%)	7 (5%)	7 (5%)	2	19
45	CN	192/200 (96%)	168 (88%)	18 (9%)	6 (3%)	4	27
46	Ca	142/144 (99%)	101 (71%)	24 (17%)	17 (12%)	0	6
47	CQ	161/188 (86%)	127 (79%)	18 (11%)	16 (10%)	0	9
48	CD	302/304 (99%)	213 (70%)	35 (12%)	54 (18%)	0	3
49	CR	187/209 (90%)	163 (87%)	14 (8%)	10 (5%)	2	19
50	CP	169/171 (99%)	140 (83%)	12 (7%)	17 (10%)	0	9
51	CX	120/152 (79%)	100 (83%)	17 (14%)	3 (2%)	5	32
52	CW	73/162 (45%)	55 (75%)	12 (16%)	6 (8%)	1	12
53	CY	128/150 (85%)	114 (89%)	8 (6%)	6 (5%)	2	21
54	Cr	71/147 (48%)	49 (69%)	13 (18%)	9 (13%)	0	5
55	Cc	110/112 (98%)	96 (87%)	10 (9%)	4 (4%)	3	25
56	Cd	118/123 (96%)	98 (83%)	8 (7%)	12 (10%)	0	8
57	Ce	131/133 (98%)	113 (86%)	10 (8%)	8 (6%)	1	16
58	Cj	92/94 (98%)	58 (63%)	19 (21%)	15 (16%)	0	3
59	Cl	49/51 (96%)	36 (74%)	8 (16%)	5 (10%)	0	8
60	Co	103/105 (98%)	76 (74%)	13 (13%)	14 (14%)	0	4
61	CM	132/134 (98%)	101 (76%)	14 (11%)	17 (13%)	0	5
62	CS	165/178 (93%)	122 (74%)	20 (12%)	23 (14%)	0	4
63	CU	106/130 (82%)	76 (72%)	13 (12%)	17 (16%)	0	3
64	Ci	75/112 (67%)	59 (79%)	5 (7%)	11 (15%)	0	4
65	CK	126/166 (76%)	94 (75%)	17 (14%)	15 (12%)	0	6
66	Cu	56/110 (51%)	54 (96%)	1 (2%)	1 (2%)	8	40
66	Cv	56/110 (51%)	53 (95%)	2 (4%)	1 (2%)	8	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	Cs	57/113 (50%)	54 (95%)	3 (5%)	0	100	100
67	Ct	57/113 (50%)	54 (95%)	3 (5%)	0	100	100
68	Ch	122/124 (98%)	103 (84%)	11 (9%)	8 (7%)	1	15
69	CF	242/244 (99%)	217 (90%)	16 (7%)	9 (4%)	3	25
70	Cq	260/319 (82%)	233 (90%)	15 (6%)	12 (5%)	2	21
71	CB	387/389 (100%)	307 (79%)	43 (11%)	37 (10%)	0	9
72	CC	368/405 (91%)	311 (84%)	27 (7%)	30 (8%)	1	12
73	CO	204/206 (99%)	179 (88%)	14 (7%)	11 (5%)	2	19
74	Cp	90/92 (98%)	81 (90%)	7 (8%)	2 (2%)	6	35
75	CI	182/224 (81%)	147 (81%)	24 (13%)	11 (6%)	1	16
76	Cn	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2	22
77	Cm	50/53 (94%)	46 (92%)	3 (6%)	1 (2%)	7	37
78	CL	206/208 (99%)	168 (82%)	13 (6%)	25 (12%)	0	5
79	CE	217/219 (99%)	177 (82%)	14 (6%)	26 (12%)	0	6
80	Cf	109/111 (98%)	103 (94%)	5 (5%)	1 (1%)	17	56
81	Ck	67/69 (97%)	63 (94%)	2 (3%)	2 (3%)	4	28
82	Cb	56/60 (93%)	48 (86%)	4 (7%)	4 (7%)	1	14
83	Cg	108/119 (91%)	96 (89%)	8 (7%)	4 (4%)	3	25
All	All	11663/13543 (86%)	9641 (83%)	1083 (9%)	939 (8%)	2	12

5 of 939 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	BY	2	ALA
4	BY	39	ASN
4	BY	41	SER
4	BY	46	LYS
4	BY	49	LEU

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	BY	116/116 (100%)	110 (95%)	6 (5%)	23	49
5	BI	56/179 (31%)	53 (95%)	3 (5%)	22	49
6	BK	90/146 (62%)	88 (98%)	2 (2%)	52	71
7	BM	101/142 (71%)	101 (100%)	0	100	100
8	Bf	62/135 (46%)	60 (97%)	2 (3%)	39	61
9	BX	113/113 (100%)	111 (98%)	2 (2%)	59	77
10	Bg	323/323 (100%)	310 (96%)	13 (4%)	31	56
11	BD	175/175 (100%)	170 (97%)	5 (3%)	42	64
12	BE	176/225 (78%)	172 (98%)	4 (2%)	50	70
13	BF	159/159 (100%)	153 (96%)	6 (4%)	33	57
14	BQ	103/120 (86%)	97 (94%)	6 (6%)	20	46
15	BU	113/113 (100%)	107 (95%)	6 (5%)	22	49
16	BO	94/120 (78%)	90 (96%)	4 (4%)	29	54
17	BS	133/133 (100%)	125 (94%)	8 (6%)	19	46
18	BN	106/130 (82%)	101 (95%)	5 (5%)	26	52
19	BL	74/135 (55%)	70 (95%)	4 (5%)	22	49
20	BT	121/121 (100%)	115 (95%)	6 (5%)	24	50
21	BP	77/130 (59%)	71 (92%)	6 (8%)	12	38
22	BZ	87/93 (94%)	84 (97%)	3 (3%)	37	60
23	Bc	52/58 (90%)	48 (92%)	4 (8%)	13	39
24	BW	113/113 (100%)	109 (96%)	4 (4%)	36	60
25	Bd	40/47 (85%)	39 (98%)	1 (2%)	47	68
26	Bb	78/78 (100%)	78 (100%)	0	100	100
27	Be	47/49 (96%)	46 (98%)	1 (2%)	53	72
28	BA	161/204 (79%)	153 (95%)	8 (5%)	24	50
29	BR	105/127 (83%)	103 (98%)	2 (2%)	57	75
30	BB	188/226 (83%)	186 (99%)	2 (1%)	73	84
31	BV	63/68 (93%)	59 (94%)	4 (6%)	18	44
32	Ba	80/107 (75%)	78 (98%)	2 (2%)	47	68
33	BJ	160/167 (96%)	157 (98%)	3 (2%)	57	75
34	BC	182/211 (86%)	177 (97%)	5 (3%)	44	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	BG	201/210 (96%)	192 (96%)	9 (4%)	27	53
36	BH	164/168 (98%)	157 (96%)	7 (4%)	29	54
37	CG	205/220 (93%)	194 (95%)	11 (5%)	22	49
38	CT	139/141 (99%)	135 (97%)	4 (3%)	42	64
39	CZ	113/113 (100%)	109 (96%)	4 (4%)	36	60
40	Cz	192/192 (100%)	182 (95%)	10 (5%)	23	49
41	CA	195/199 (98%)	184 (94%)	11 (6%)	21	47
42	CJ	149/157 (95%)	139 (93%)	10 (7%)	16	42
43	CH	164/164 (100%)	158 (96%)	6 (4%)	34	58
44	CV	109/109 (100%)	106 (97%)	3 (3%)	43	65
45	CN	167/173 (96%)	161 (96%)	6 (4%)	35	59
46	Ca	110/110 (100%)	101 (92%)	9 (8%)	11	36
47	CQ	138/160 (86%)	132 (96%)	6 (4%)	29	54
48	CD	251/251 (100%)	234 (93%)	17 (7%)	16	42
49	CR	166/183 (91%)	154 (93%)	12 (7%)	14	41
50	CP	144/144 (100%)	139 (96%)	5 (4%)	36	60
51	CX	109/130 (84%)	102 (94%)	7 (6%)	17	44
52	CW	66/133 (50%)	65 (98%)	1 (2%)	65	80
53	CY	115/128 (90%)	110 (96%)	5 (4%)	29	54
54	Cr	64/131 (49%)	61 (95%)	3 (5%)	26	52
55	Cc	98/98 (100%)	94 (96%)	4 (4%)	30	55
56	Cd	103/106 (97%)	98 (95%)	5 (5%)	25	51
57	Ce	122/122 (100%)	116 (95%)	6 (5%)	25	51
58	Cj	77/77 (100%)	74 (96%)	3 (4%)	32	57
59	Cl	48/48 (100%)	47 (98%)	1 (2%)	53	72
60	Co	94/94 (100%)	87 (93%)	7 (7%)	13	40
61	CM	116/116 (100%)	110 (95%)	6 (5%)	23	49
62	CS	153/163 (94%)	145 (95%)	8 (5%)	23	49
63	CU	94/106 (89%)	86 (92%)	8 (8%)	10	35
64	Ci	62/92 (67%)	59 (95%)	3 (5%)	25	52
65	CK	105/139 (76%)	98 (93%)	7 (7%)	16	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	Cu	46/77 (60%)	45 (98%)	1 (2%)	52	71
66	Cv	46/77 (60%)	46 (100%)	0	100	100
67	Cs	48/82 (58%)	47 (98%)	1 (2%)	53	72
67	Ct	48/82 (58%)	46 (96%)	2 (4%)	30	54
68	Ch	109/109 (100%)	103 (94%)	6 (6%)	21	48
69	CF	206/206 (100%)	199 (97%)	7 (3%)	37	60
70	Cq	222/265 (84%)	216 (97%)	6 (3%)	44	65
71	CB	335/335 (100%)	315 (94%)	20 (6%)	19	46
72	CC	302/329 (92%)	286 (95%)	16 (5%)	22	49
73	CO	173/173 (100%)	160 (92%)	13 (8%)	13	39
74	Cp	73/73 (100%)	72 (99%)	1 (1%)	67	80
75	CI	156/183 (85%)	152 (97%)	4 (3%)	46	67
76	Cn	24/24 (100%)	23 (96%)	1 (4%)	30	54
77	Cm	47/48 (98%)	46 (98%)	1 (2%)	53	72
78	CL	175/175 (100%)	166 (95%)	9 (5%)	24	50
79	CE	185/185 (100%)	169 (91%)	16 (9%)	10	34
80	Cf	96/96 (100%)	93 (97%)	3 (3%)	40	62
81	Ck	63/63 (100%)	58 (92%)	5 (8%)	12	38
82	Cb	51/53 (96%)	51 (100%)	0	100	100
83	Cg	98/107 (92%)	91 (93%)	7 (7%)	14	41
All	All	10084/11382 (89%)	9634 (96%)	450 (4%)	31	53

5 of 450 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	CD	203	HIS
83	Cg	9	LYS
57	Ce	121	THR
81	Ck	1	MET
73	CO	152	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 129 such sidechains are listed below:

Mol	Chain	Res	Type
75	CI	14	ASN
79	CE	67	HIS
35	BG	160	ASN
35	BG	59	GLN
80	Cf	26	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Ad	1760/1810 (97%)	458 (26%)	0
2	Ae	74/75 (98%)	19 (25%)	0
3	Af	10/11 (90%)	2 (20%)	0
84	Aa	3389/3391 (99%)	748 (22%)	0
85	Ac	159/160 (99%)	35 (22%)	0
86	Ab	119/120 (99%)	23 (19%)	0
All	All	5511/5567 (98%)	1285 (23%)	0

5 of 1285 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Ad	4	C
1	Ad	8	U
1	Ad	16	G
1	Ad	25	C
1	Ad	26	A

There are no RNA pucker outliers to report.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

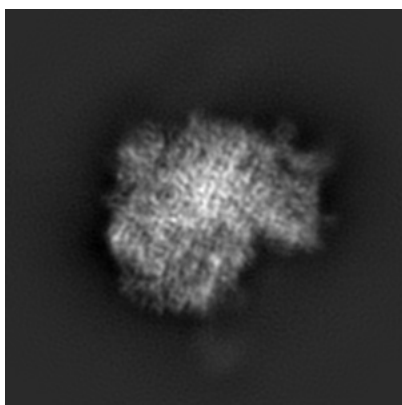
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1780. These allow visual inspection of the internal detail of the map and identification of artifacts.

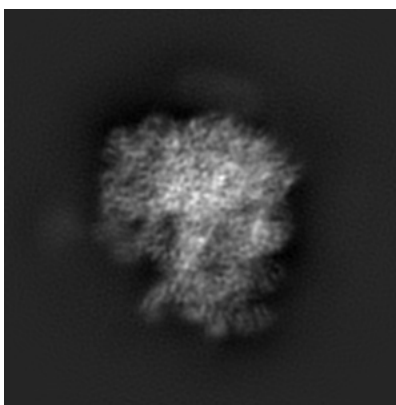
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

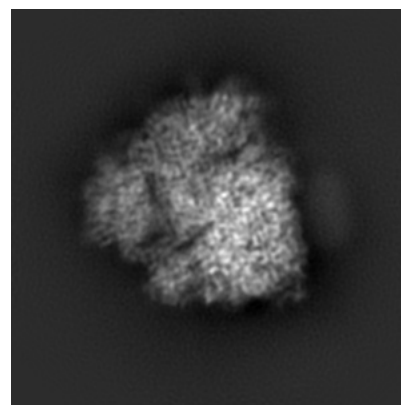
#### 6.1.1 Primary map



X



Y

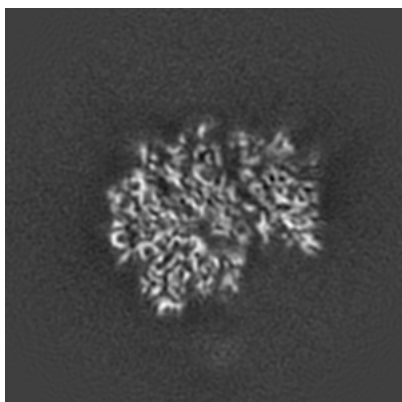


Z

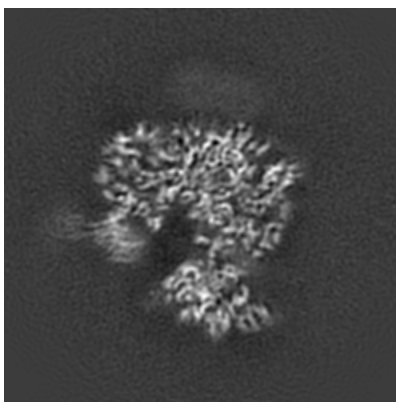
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

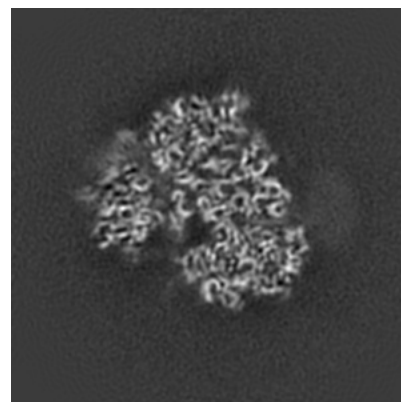
#### 6.2.1 Primary map



X Index: 184



Y Index: 184



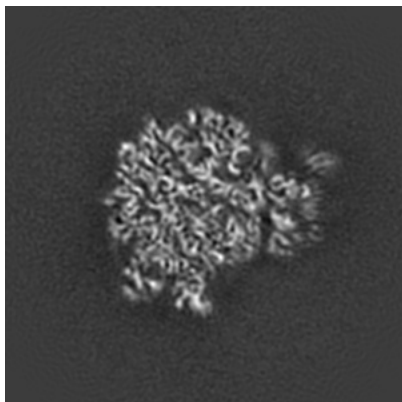
Z Index: 184



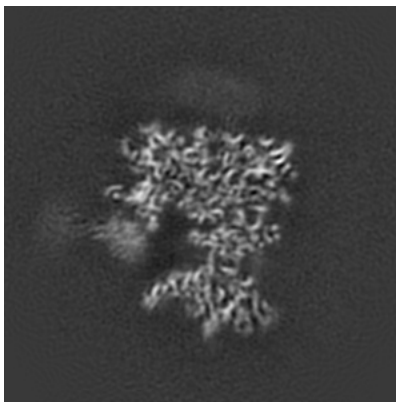
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

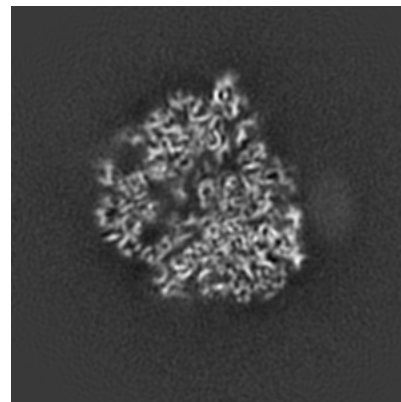
### 6.3.1 Primary map



X Index: 213



Y Index: 193

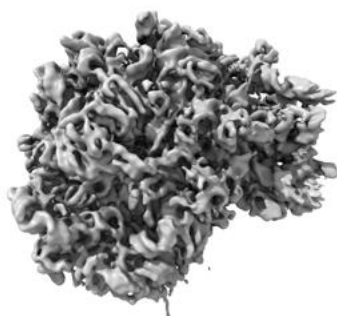


Z Index: 173

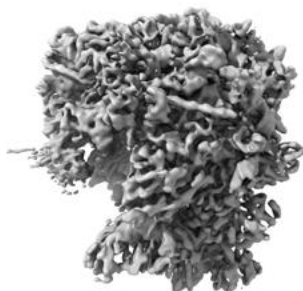
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

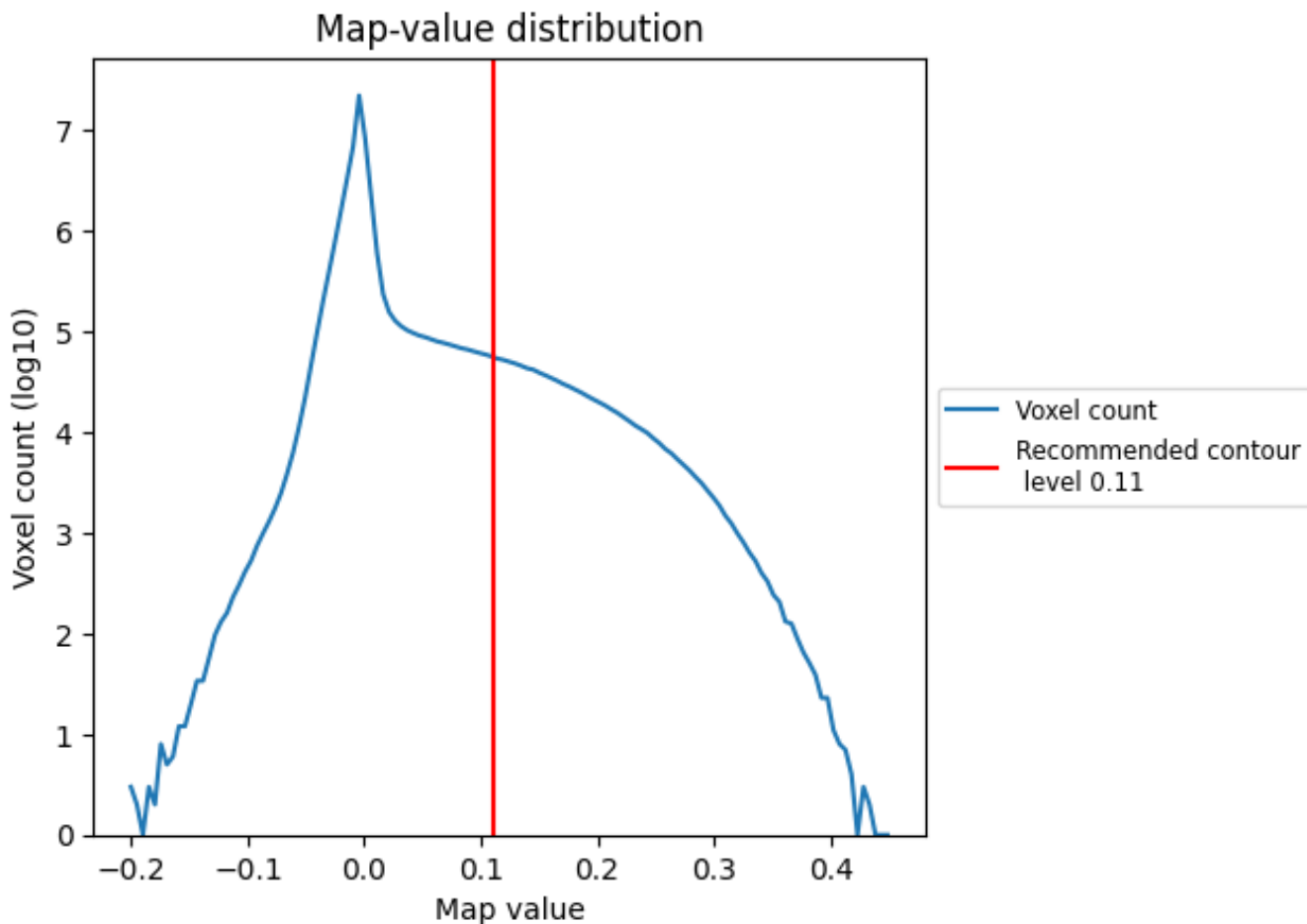
## 6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

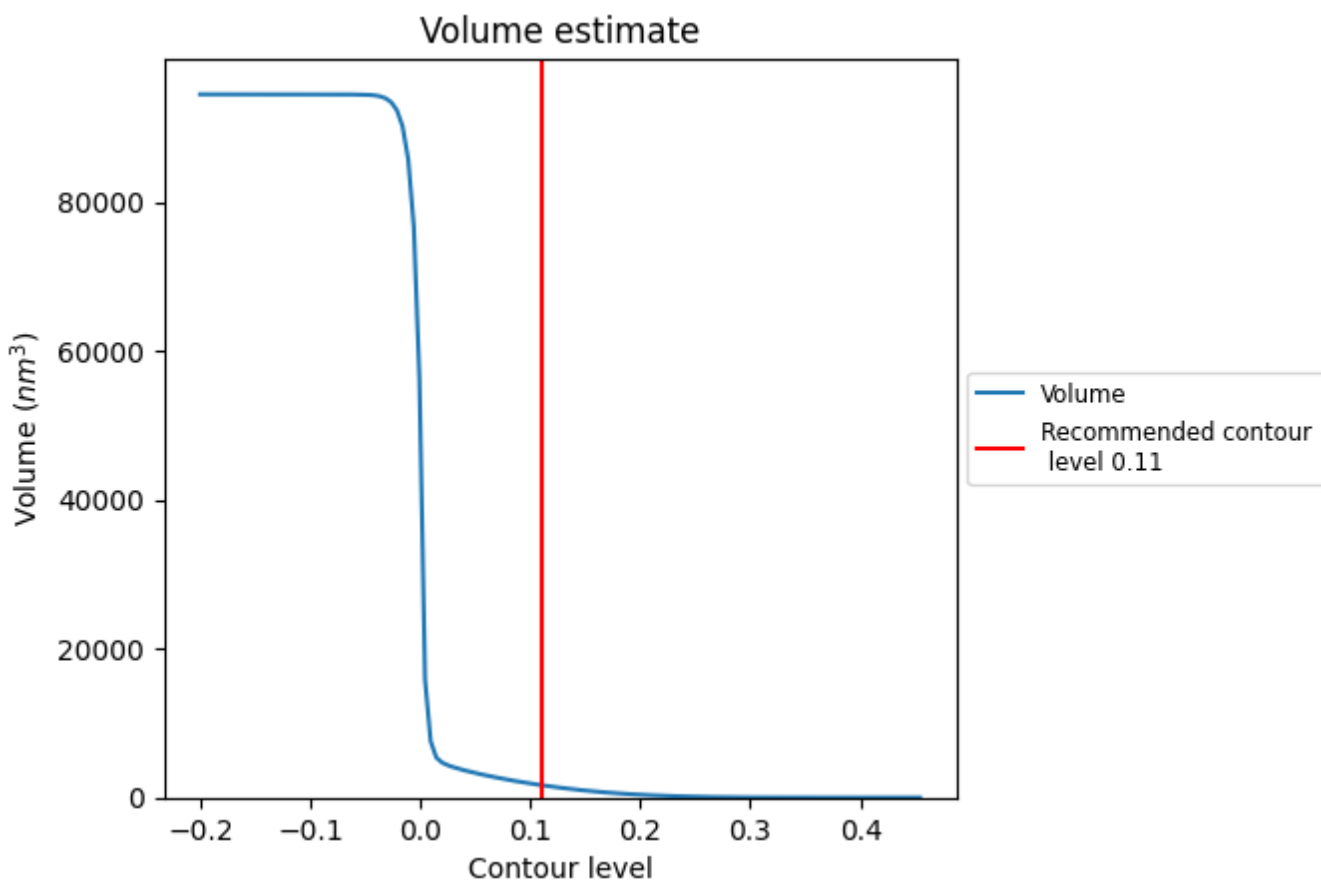
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

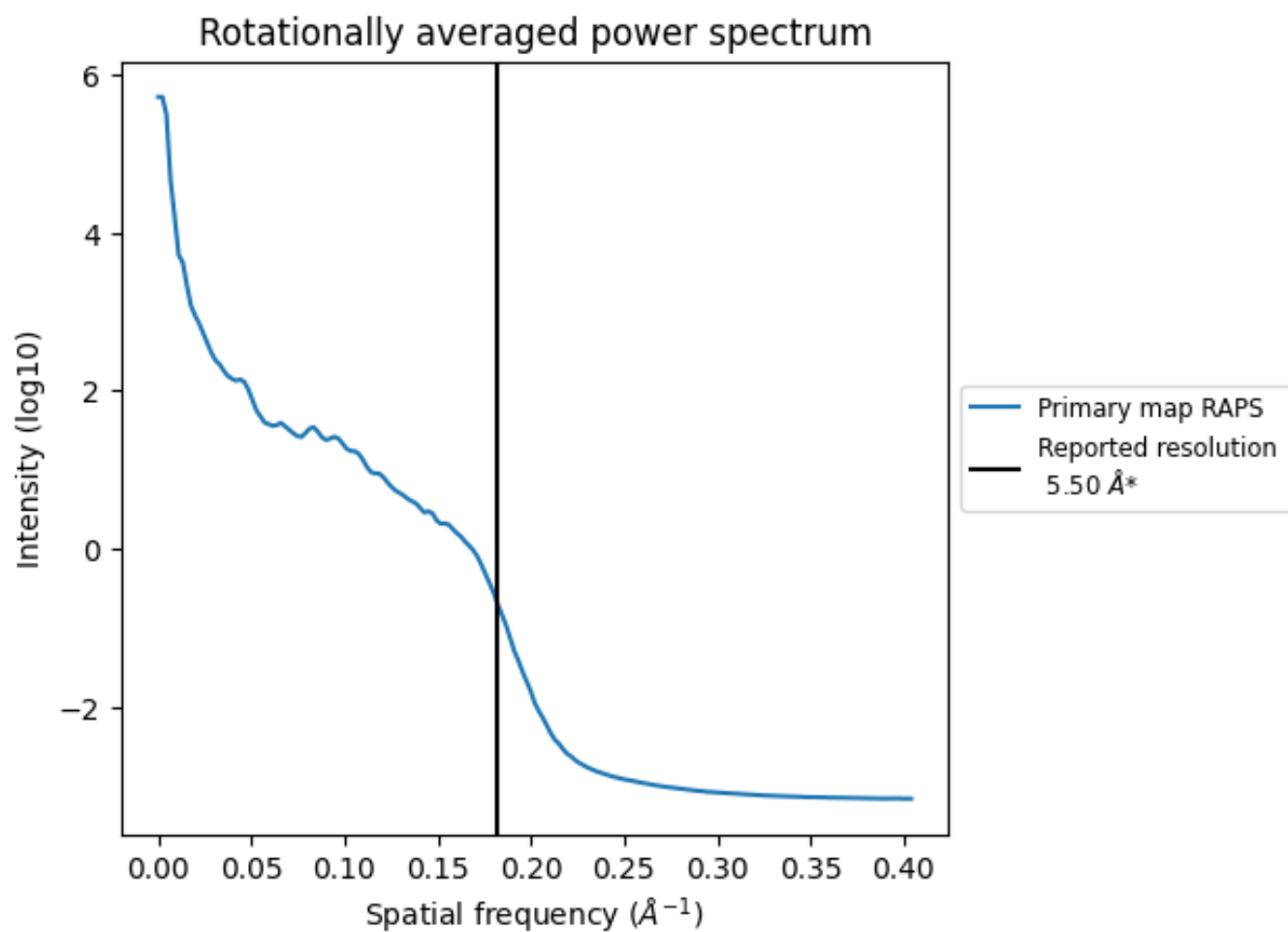
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1668 nm<sup>3</sup>; this corresponds to an approximate mass of 1506 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.182 \text{\AA}^{-1}$

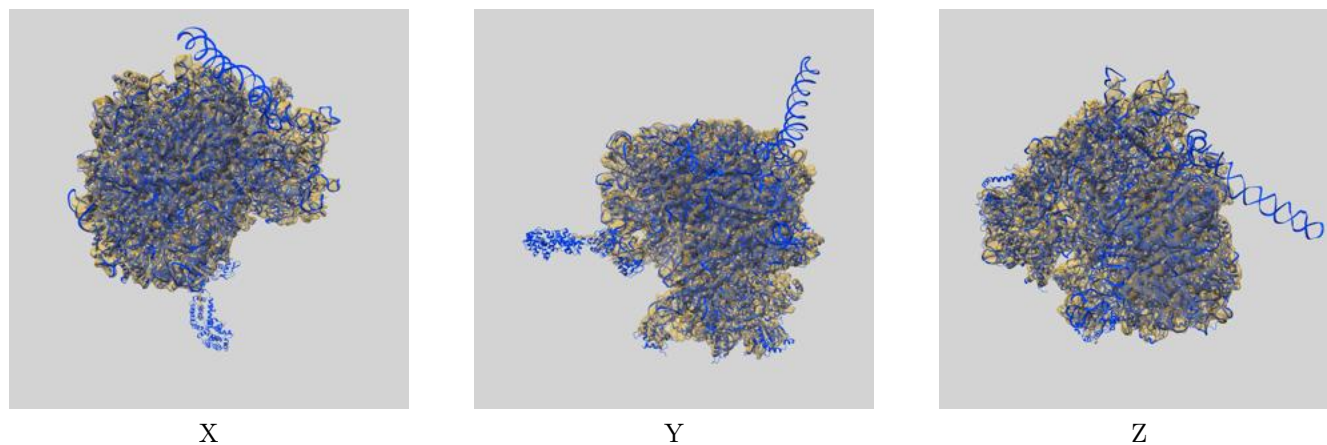
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

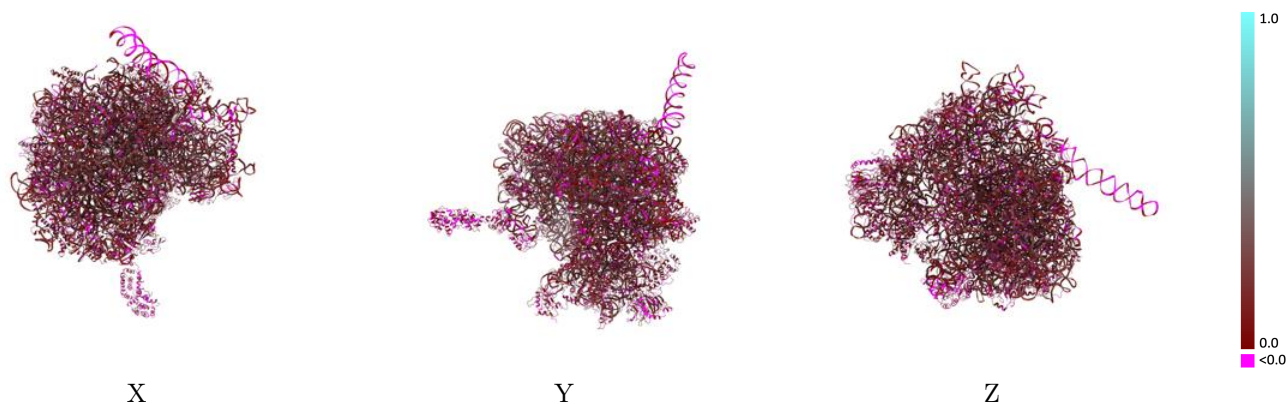
This section contains information regarding the fit between EMDB map EMD-1780 and PDB model 4V7E. Per-residue inclusion information can be found in section 3 on page 20.

### 9.1 Map-model overlay [i](#)



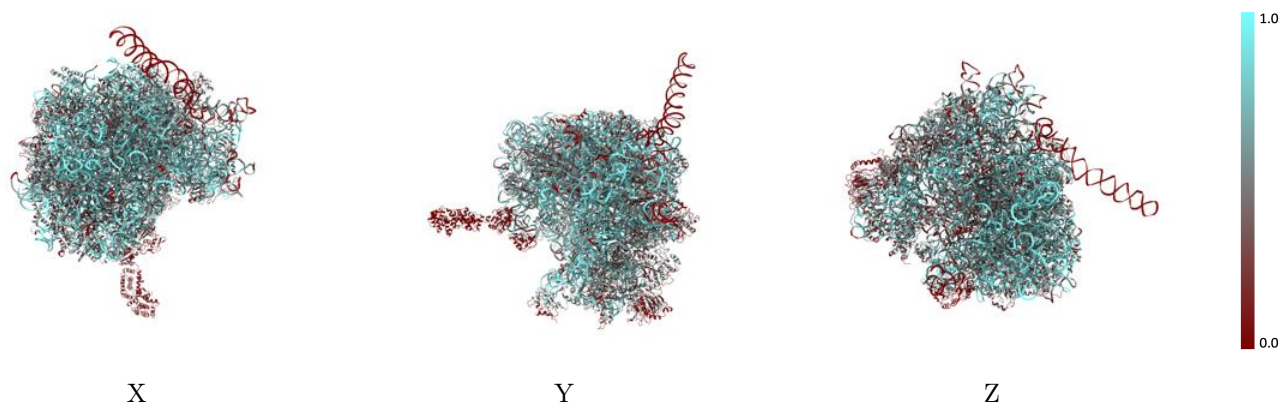
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

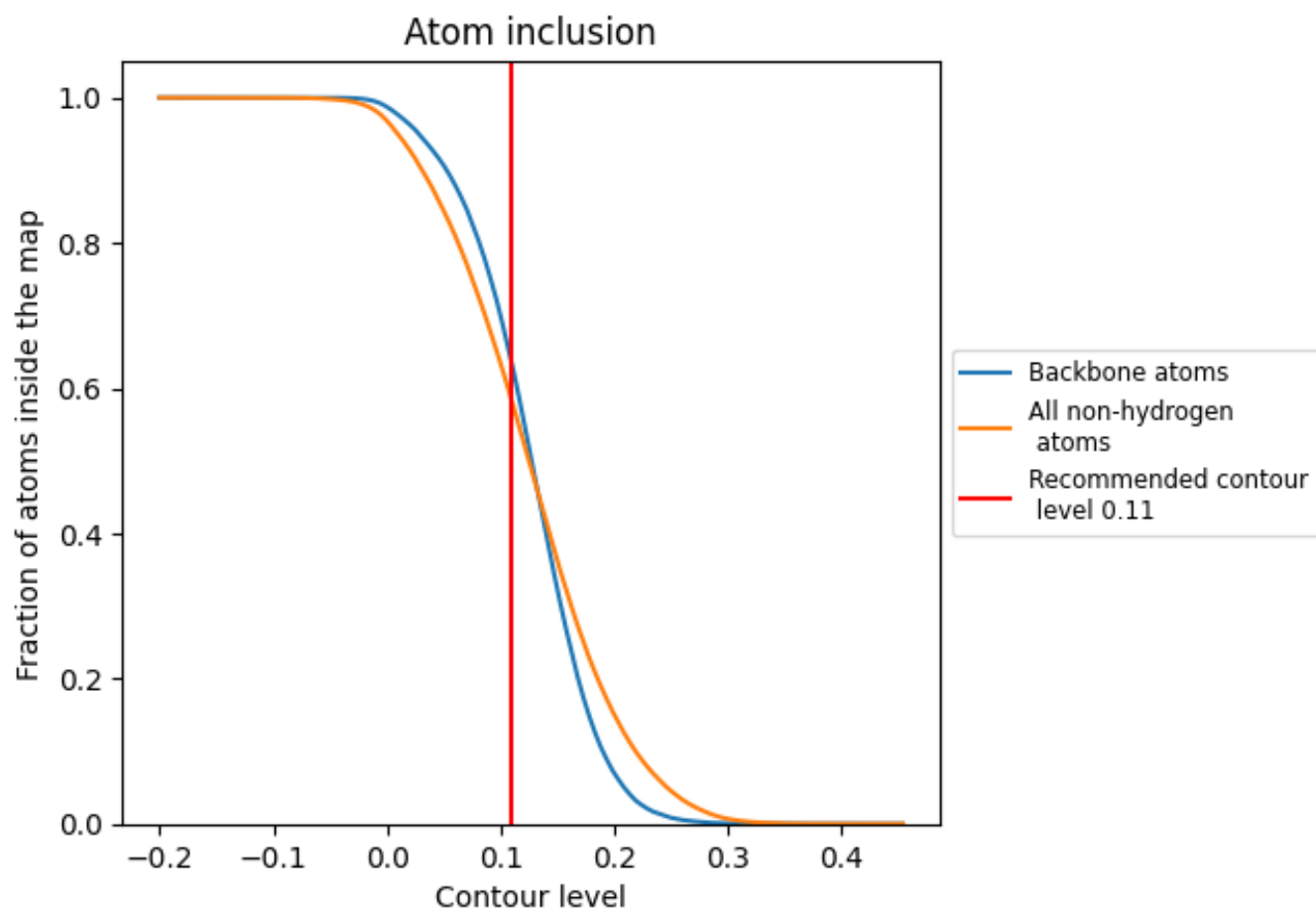
## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.11).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5826	 0.1550
Aa	 0.7377	 0.1940
Ab	 0.8528	 0.2080
Ac	 0.7934	 0.2070
Ad	 0.7396	 0.1960
Ae	 0.4915	 0.1860
Af	 0.1293	 0.0800
BA	 0.3804	 0.1240
BB	 0.4210	 0.1260
BC	 0.3646	 0.1210
BD	 0.3293	 0.1190
BE	 0.4311	 0.1040
BF	 0.4542	 0.1280
BG	 0.4302	 0.1120
BH	 0.3666	 0.1230
BI	 0.4139	 0.1110
BJ	 0.4894	 0.1170
BK	 0.4180	 0.0950
BL	 0.3153	 0.1070
BM	 0.2871	 0.0870
BN	 0.3866	 0.0980
BO	 0.3839	 0.1130
BP	 0.4370	 0.1110
BQ	 0.3975	 0.0950
BR	 0.3454	 0.1130
BS	 0.4000	 0.1130
BT	 0.4459	 0.1070
BU	 0.3075	 0.0920
BV	 0.3601	 0.1050
BW	 0.3448	 0.0840
BX	 0.4157	 0.1190
BY	 0.4148	 0.0740
BZ	 0.3447	 0.0990
Ba	 0.4599	 0.1350
Bb	 0.4000	 0.1200



























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Chain	Atom inclusion	Q-score
Bc	0.3077	0.0630
Bd	0.3736	0.0680
Be	0.3031	0.0730
Bf	0.3569	0.0730
Bg	0.2151	0.0850
CA	0.3965	0.1150
CB	0.4292	0.1080
CC	0.4029	0.1160
CD	0.4762	0.1050
CE	0.3678	0.0960
CF	0.4640	0.1200
CG	0.4751	0.1180
CH	0.4758	0.1140
CI	0.4448	0.1210
CJ	0.4656	0.1300
CK	0.0583	0.0530
CL	0.4417	0.1020
CM	0.4739	0.1230
CN	0.4819	0.1090
CO	0.4495	0.1070
CP	0.4274	0.1150
CQ	0.4246	0.1150
CR	0.4299	0.1140
CS	0.4637	0.1040
CT	0.3952	0.1130
CU	0.3175	0.0650
CV	0.2652	0.1300
CW	0.2757	0.1230
CX	0.3930	0.1120
CY	0.5448	0.1270
CZ	0.5066	0.1270
Ca	0.4074	0.0920
Cb	0.3613	0.0940
Cc	0.4303	0.1090
Cd	0.4082	0.0930
Ce	0.3661	0.1060
Cf	0.4198	0.0960
Cg	0.4448	0.1210
Ch	0.4536	0.0910
Ci	0.4105	0.0870
Cj	0.4672	0.1040
Ck	0.4709	0.1140

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Chain	Atom inclusion	Q-score
Cl	 0.4312	 0.1180
Cm	 0.5290	 0.1580
Cn	 0.2831	 -0.0170
Co	 0.3911	 0.0940
Cp	 0.3991	 0.1240
Cq	 0.0737	 0.0580
Cr	 0.4893	 0.1140
Cs	 0.0137	 0.0590
Ct	 0.0000	 0.0300
Cu	 0.0000	 0.0430
Cv	 0.0000	 0.0280
Cz	 0.0260	 0.0410